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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Identification of novel e2f target genes Patent: WO 2004035798-A 1817 29-APR-2004,
CropDesign N.V. (BE)
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                 nucleic search, using frame_plus_p2n model
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Database

Result No.

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Plant Bioscience Limited (GB)
Location/Qualifiers
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                                                             ThrvalProAspGlyHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrp
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/product="reduced vernalization response 1"
/product="reduced vernalization response 1"
/protein id="AAM76973.1"
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KRTVTAEERERAINAAKTFEPTNPFRYVLRPSVLYRGCIMYLPSGFAEKYLSGISGF
RKVQLAEKOWPRCLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTR
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VRN1, a gene required for response to vernalization Unpublished
Jacob (bases 1 to 1538)
Levy, Y. Y. and Dean, C.
Direct Submission
Submitted (13-JUL-2000) Molecular Genetics, John Innes Centre, Colney Lane, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                   /note="contains two VP1/ABI3-like B3 domains"
/codon_start=1
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Matches:
Conservative:
Mismatches:
Indels:
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/ecotype="Landsberg erecta"
1. 1538
/gene="VRN1"
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/chromosome="3"
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/gene="VRN1"
/allele="Ler"
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Arabidopsis thaliana reduced vernalization response 1 (VRN1) mRNA,
VRN1-Ler allele, complete cds.
AP289052.1 GI:21734795
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                            ArgleuPheGluAspLeuGluAspGluAspAlaGluValIlePheProSerSerValTyr
                                                                 CGTTTGTTTGAAGACCTTGAAGATGAAGATGCCGAGGTCATCTTTCCTTCTTCTGTGTAC
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Levy, Y.Y., Gendall, A.R. and Dean, C.
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Arabidopsis thaliana
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Arabidopsis thaliana reduced vernalization response 1 (VRN1) gene, AP289051
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 5000)
Levy, Y.Y., Mesnage, S., Mylne, J.S., Gendall, A.R. and Dean, C.
Multiple roles of Arabidopsis VRN1 in vernalization and flowering
time control
Science 297 (5579), 243-246 (2002)
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                   LysLysArgGlyArgLysLysAsnAlaAspProGluGluIleAsnSerSerAlaPro
                                                                                                                                                  221 ThrValThrAlaGluGluArgGluArgAlaIleAsnAlaAlaLysThrPheGluProThr
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                                      809 AAAAAGAGAGGAAGGAAGAAGAA-AATGCTGATCCTGAGGAAATAAACTCATCAGCTCCG
                                                                                 201 ArgAspAspAspProGluAsnArgSerLysPheTyrGluSerAlaSerAlaArgLysArg
                                                                                                                 868 CGAGATGATCCAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGA
                                                                                                                                                                                   928 ACCGTGACTGCAGAAAGAGAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCAAACA
                                                                                                                                                                                                                  241 AsnProPhePheArgValValLeuArgProSerTyrLeuTyrArgGlyCysIleMetTyr
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Levy, Y.Y. and Dean, C.

Levy, Y.Y. and Dean, C.

Submisted (23-JUL-2000) Molecular Genetics, John Innes Centre, Colney Lane, Norwich, Norfolk NR4 7UH, UK

Location/Qualifiers

1. 5000

/organism="Arabidopsis thaliana"
/MD trye="genomic DNA"
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/chromosome="3"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="vrn1-2 mutation"
                                                                                                 DNA
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Patent: WO 0121822-A 13 29-MAR-2001;
Plant Bioscience Limited (GB)
Location/Qualifiers
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3 Expense 13 from Patent W00121822

AX101039

AX101039.1 GI:13619895
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DNA Res. 7 (3), 217-221 (2000)
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Arabidopsis thaliana
Bubaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Direct Submission
Submitted (18-NOv-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research, 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
                                                                                                        ----GluGluIle 195
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AATGCTGATCCTGTTTTCAGAGGACTCTTTTCAGAGGA
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frvolaekywpyrclyvytky
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9
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                             gene
                                                                          mRNA
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4319

325

4199

285

305

us-10-088-187a-11.rge

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REHMIKAPKEYLPLMIJTSEYRICPVSINLQGDVFSVULKRELSLPDPDYSHQFDIGRV
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AVCCERWLEPQEHHRYQCRREYKITDKIYILGEDNKVDEVGSGGGGATDSLEGISQVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLSDSKCLESIQAHDDAINTVAAGFDDLLFTGSADGTLKVWKRELQGKGTKHFLVNVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTLKEFLTKSVNPKNYVEVRRRKNVLKIRHYDAVSCLSLNEELGLLYSGSWDKTLKVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25146. .26393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to unknown protein"
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similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="tRNA-Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
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'evidence=not ∈
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/note="gb|
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Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=Kl3El3
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiaes. Genes that have no significant protein similarity are described as 'unknown protein.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://CCm.081.mit.edu/GENSCAN.html), NetGenes (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGenes/) and SplicePredictor (Volker Brendel, Stanford University, Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE)
This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MCB22 and the 3' clone is MHP21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WIKSYKLLCYYRGTKYFEIYDEDSDSWILLDDIIAPRGSIGYSELSYSLKGWYWFAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /trānslation="METVVEEGKLVNEDCSTLVLPALSIGNVGQLAVDLLVSSTGAER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join (5713. .5792,5883. .6006,6112. .6349,6579. .6697,6873. .6931,7161. .7336,7623. .7662))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (2742. .3977)
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gene id:Kl3813.2
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Bimilar to unknown protein"
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QY         169	Oy 260
LINYAPSILVOIEQAGGGKTKRGDD"  COMPIEMENT (join (2770927957,2804828247,2834728409, 2851228692))  // note="unmaned protein product; gp AAD43153.1  gene jd:K13E13.10  similar to unknown protein" // coin start=1 // evidence=not experimental // protein id="EAB01695.1" // Ab xref="G1:2280316" // Coin start=1 // Ab xref="G1:2280316" // Ab xref="G1:2280316" // Coin start=1 // Coin start=1 // Coin start=1 // Coin start=1 // Ab xref="G1:2380316" // Ab xref="G1:3280316" // Ab xref="G1:3280317" // Ab xref="	Alignment Scores:  15.98e-122   Length: 321 Score:  50.001 Score:  15.4.50   Conservative: 0 Score:  17.16*   Mismatches: 0 Score:  18.99*   Gaps: 321 Score:  18.91*   Mismatches: 0 Score: 0 S

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                                                                                                                                                                                                                                                                                                                          4260 TTCACTCTAGAGAACAACTTAGGAGAAGAGAGACGTCTGTGTGTTTGAGCTGCTCAGAACC 4319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AY517929
Brassica rapa cultivar Kwonsim reduced vernalization response 1
                                                                                                                                                                                                                                                       4200 TGGCCTGTTCGATGTCTCTGACAAAGCCGGGAGAGCCAAATTCAGTCAAGGATGGTACGAA 4259
                                                                                                                                                                                             4140 GCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAGTCCAGCTTGCGGAGAAACAA 4199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots; tosidas, eurosida II; Brassicales; Brassicaceae; Brassica.

(bases 1 to 990)

(Kwon, S.-J., Park, B.-S., Kim, S.-Y., Choi, H.-S., Lee, M.-C., Kim, S.-J., Park, B.-S., Lim, K.-B., Kim, J.-A., Lee, M.-R., Jin, Y.-M., Kim, J.-S., Lee, M.-R., Jin, Y.-M., Kim, J. and Kim, H.-I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kwon,S.-J., Park,B.-S., Kim,S.-Y., Choi,H.-S., Lee,M.-C.,
Kim,J.-S., Lee,S.-I., Lim,K.-B., Kim,J.-A., Lee,M.-R., Jin,Y.-M.
Kim,D. and Kim,H.-I.
Direct Submission
Submitted (Gs-DEC-2003) Genomics Division, National Institute of Agricultural Biotechnology, Seedun-dong 225, Suwon 441-707,
Republic of Korea
                                                                                                           AlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGlnLeuAlaGluLysGln
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                                                                                                                                                                                                                                                                                                      PheThrLeuGluhanAsnLeuGlyGluGlyAspValCysValPheGluLeuArgThr
                                                                                                                                                                                                                                                                                                                                                                                                 4320 AGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTACGTC 4367
                                                                                                                                                                                                                                                                                                                                                                            326 ArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyrVal 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica rapa Kwonsim VRN1 mRNA
Unpublished
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                                                                                       260 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA, complete cds. AY517929
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                  GlyCysileMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica rapa
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                                                                                                                                                                                                                                   286
                                                                                                                                                                                                                                                                                                       306
                    256
                                                                                                                                                            266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosida II; Brassicales; Brassicaceae; Brassica.

I (Basea I to 990)

Kwon, S.-J., Lee, M.-C.,

Kim, J.-S., Lee, S.-I., Lim, K.-B., Kim, J.-A., Hong, K.-Y., Lee, M.-C.,

Jin, Y.-M., Kim, D. and Kim, H.-I.

Direct Submission

Submitted (23-JUL-2003) Genomics Division, National Institute of Agricultural Biotechnology, Seodun-dong 225, Suwon 441-707,

Republic of Korea

Location/Qualifiers

J. . 990

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| Advaref="Raxon:3711"
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/protectin id="AAQ55453.1"
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/db_xref="di:
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on Jul 9, 1999 this sequence version replaced gi:5019265.

e-mail for correspondence: arab@sequence.stanford.edu
Genes with similarity to proteins in the databases are described
as 'putestive', 'like' or 'similar to'. Genes that have BST
similarity but no significant protein similarity are described as
'unknown proteins'. Genes that are annotated based only on gene
prediction software are described as 'hypothetical proteins'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://gonaic.stanford.edu/-chris/GENSCANW.html), Fexa (V.Solovyev
& A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/),
NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.obs.dtu.dk/NerPlantGene.html) and
eMotif(Nevill-Manning, C.G. Wu, T.D. & Brutlag, D.L.,
http://motif.stanford.edu/projects.html).
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ENIQALICTRNWLRGFPKEGEBEEVEEEKBEEKEERER
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                                                                                                          1 (bases 1 to 125021)
Pederspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Palm, C.J., Edward, D., Buehler, E., Dunn, P., Altafil, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission Bond Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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7840. .8514,8612. .8939,9020. .9240,9369. .9546,9658.
/gene="Pl3F21.2"
Direct Submission
Submitted (06-MAY-1999) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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/mol type="genomic DNA"
/db_xref="taxon:3702"
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note="Hypothetical Protein"
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 125021)
Federspiel, N. P. Palm. C.J., Conway, A.B., Conn, L., Hansen, N.F.,
Altafi, H., Araujo, R., Huizar, L., Rowley, D., Euchler, E., Dunn, P.,
Altafi, H., Araujo, R., Huizar, I., Kim, C., Lenz, C., Li, J., Liu, S.,
Luros, S., Schwartz, J., Shinn, P., Toriuni, M., Vysocekaia, V.S.,
Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
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                                                                                   uAspleuGluAspGluAspAlaGluValllePheProSerSerValTyrProSerProLe 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
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gene

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/gene="F13F21.5"
complement(join(15762. .15977,16061. .16492,16809. .16883))
                                                                                                                                                                          ALGFYGGHWSPNSLSILAHGYGGAFHLWRNVSSSKESENWQMOKVPSGHFAAYTDVTW
ARTGEVLLSVSQDQTTRYFSARKDDEGNBAEDEHWHELARPOYHGHDINCVAMVQKG
NHRFYSGAEEKVVRVFEAPLSFLKTHNTCAGGEGSFPEDLQADVQULGANWSALGLS
OKPIYLHSSSEPLEARNGGEGLDTFETVPEAAPAELKEPPIBDQLAFHTLWPESHKLY
GHGNELFSLCSDHKGNLVASSCKAGSASMAETWLWEVGTWKAVGRLOSHSLTYTHLEF
SYDDTLLLSVSKBDRFFSVFSIQFTDMEVSTKAKVGRLOSHSLTYTHLEF
SSRDKTYKTKIWSVENDARIKQILVLPPFGSSVTRVAWTGLDRMEKSGCVAVGMSSGLIE
LSNVKIIETEEGTTATAALALRLEPFMCHVSAVNRLAWRPTEKCESNQSLRWLTSCGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon start=1
/product="geranyl geranyl pyrophosphate synthase"
/product="geranyl geranyl pyrophosphate synthase"
/protein_id="AaDa148.1"
/db_xref="id=$410748"
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KALDNSIPLCNNFVPFWEPVLEVHKAMRYTLLPGGKRVRPMLCLVACELVGGGESTAM
PAGAVENIHAASLILDDLPCNDDDSIRRGKFPNHKVPGERKTSILASNALRSIAVKQT
IAASTSLGYTSERVLRAVORMARAYGTEGLVAGQAADLAGERNSFKNEDDELRYLELMH
VHKTATLVEAAAVVQBAIMGGGSDBEIRRLKSYARCVGIMFQVMDDVLDETKSSEBLGK
TAGKDLITGKLTYPRVMGVDNAREYAKRINREAQEHLQGFDSDKVVPLLSLADYIVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAD43151.1"
/db_xref="GI:5430751"
/translation="MYTLKWEICIELLKLTVDFVAAVAESIEVAFRHRPPPVIQYSSV
MYGRRSMYTAVPIPLVGFL"
23803. .26346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Hypotherical Protein"
/codon_start=1
/protein_id="AAD43149.1"
/db_xref==[d1:5430749"
/fab_xref==[d1:5430749"
/translation="MVSDSDIVTQLREILRSSDLETTTPASVRRQLEVYFGVELTDKK
AFVRRQLBAFLESSDALLESKPRQEEEDOWGDQNDEEGSENDDDKTELPYKAKKRGGGF
NKICQLSPQLEKFLGTSQLARTEVVKKWMAYIREHDLQDPTNRRNILCDESLHSLRRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTINMFOMNKALAKHIWALNDGDGCFRAVKEEDVDETSGERDEKDVKIEBEALENNEEE
SKEEDRSVRKRKRKRKRKPAKSEEKPKKKGGGFTKVCSLSPELQAFGTPQLAKTEVV
KMLKYIKENNLQDPSDKRTIICDESLRSLFPVBSINMFOMNKQLAKHIWPLVQEDEA
GTINDPEKGKQRAKMETDBVKVNIKSSTFLNYIDNDESNEEKATSSRIKTEE"

COMPLEMENT (15762. . 16883)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /proteIn id="AAD43150.1"
/db_xref="G1:5430750"
/db_xref="G1:543075
ALALGGLDNKIKLYSGERTGKFTSVCELKGHTDWIRSLDFSLPLHTTEEIPNSIMLYS
SSQDKVIRIWKLVLVGDVGSWRREITLASYIEGPVFVSGTFTYQISVESVLIGHEDWV
YSVEWQPPVIDFIDGRLVNHQPLSILSASMDKTYMIMRPEKKTGVWVNVVCVGELSHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (join(12218, .12318,12359, .12418,12518, .12695, 12784, .12898,12987, .13143,13236, .13410,13500, .13602,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="97% identical to geranyl geranyl pyrophosphate synthase [Arabidopsis thaliana] gi|2578822."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Unknown protein; Location of ests 164G18T7
(gi|2764114), 114G10T7 (gi|2597578), and 114G11T7
(gi|2597579)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Unknown Protein; Location of ests VBVQD12
(gi[757594 and gi|757593)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F13F21.3"
complement(10370..11380)
/gene="F13F21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (10370. .11380)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (12218. .14173)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FWYKKTRNTSGNPLQNHSLETE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F13F21.6"
21730. .21921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F13F21.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F13F21.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F13F21.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="F13F21.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .14173))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNCVRVFNFKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28233 GAGCTITCAGTIGITTITIGCACTIACAAIACCTGAIGGICAIGITIG-CAIGIAGAACTA 28291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCTACTGAACCAGTGAATAAAGGTTATGGCGGTTCTACAGCCATCCAAAGCTTTTTCAA 28609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INKVDPNLKFENDRLKRAYIALQAWKKAIYSDPFKTTANWVGSDVCSYNGVYCAPALD
DDSLTVVAGVDLNHADIAGHLPPELGLMTDLALFHINSNRFCGIIPKSLSKLALMYEF
                                                                                                                                                                                     translation="MERPFGCFFILLLISYTVVATFDDEPSFPENADLTKDLEQKCFS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 uSerThrValProAlaAsnLysGlyTyr---AlaSerSerAlaIleGlnThrLeuPheTh 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28352 TCCATTCGGATTGGT-----TTCAGATACAA------GTTACAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 rGlyProValLysAlaGluGluProThrProThrProLyslleProLysLysArgGlyAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArglysAlaAspAsnLysIleTrpPheGlnAspGlyTrpGlnGluPheValAspArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluLeuSerValAlaValAlaLeuThrValProAspGlyHisValTrpArgValGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerileArgileGlyTyrLeuLeuIlePheArgTyrGluGlyAsnSerAlaPheSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 TyrilePheAsnLeu---Ser-HisSerGluIleAsnTyrHisSerThrGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uGluAspGluAspAlaGluValIlePheProSerSerValTyrProSerProLeuProGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(28449. _28680,28766. .28965,29065. .29313)
/gene="F13F21.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125021
244
22
25
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                           'note="Hypothetical Protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-088-187A-11 (1-341) x AC007504 (1-125021)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
                                                                                                                          /protein_id="AAD43152.1"
/db_xref="G1:5430752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /proteIn_id="AAD43153.1"
/db_xref="G1:5430753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="Unknown Protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28449. .29313
/gene="F13F21.8"
   23803. .26346
/gene="F13F21.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
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1098.00
70.18%
64.38%
61.14%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28550
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CDS
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Percent Similarity: 87.18\$   Conservative: 14		S17 GTGAGGTGCC  S17 GTGAGGTGCC  308 LeuGluAsnA  328 PheValLeuL  328 PheValLeuL  33 PheValLeuL  34 PL
Qy         185 gLysLysLysAsnAlaAsp-Pro	Qy         260	RESULT 13 AX50578 AX50578 LOCARIOR Sequence 273 from Patent W00216655. ACCESSION AX505578

16912

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Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                 16733 AGTTTACTTTTTATGATCTGGTAATCGAAAAAATGAATTTTCTCATCAATGTAATTTGCA
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                                                                           -----LysLysArgGlyArgLysLysAsnAlaAspProGluGluIle-
                 --LysilePro-
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                                                      Chases 1 to 78589)
Sato, S.
Direct Submission

Department of Plant Gene Research; 2-6-7 Kazusa DNA Research Institute,
Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
Chiba 292-0818, Japan (B-mail:ssato@kazusa.or.jp,
URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
Fax:81-418-52-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 HisPheLysArgAlaArgLeuPheGluAspLeuGluAspGluAspAlaGluValIlePhe 135
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Query Match:
            DNA Res. 3
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                                                        REFERENCE
AUTHORS
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Submitted (13-AUG-2004) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
On Aug 3, 2004 this sequence version replaced gi:50540779.
                                                                                                                                                                                                                                                                         Direct Submission
Submitted (03-DEC-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                   2 (bases 1 to 24377)
Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D. and Roe, B.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                      OK 73019, USA 3 (bases 1 to 243777) Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D. and Roe, B.A. Direct Submission ... Of Chemistry And Biochemi
                                                1 (bases 1 to 243777)
Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D. and Roe, B.A.
Medicago truncatula BAC Clone mth2-23j1
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the agps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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contig of 8133 bp in length
gap of unknown length
contig of 15519 bp in length
gap of unknown length
contig of 15100 bp in length
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gap of unknown length
contig of 127888 bp in length
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The University of Oklahoma
Center code:UOKNOR
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155255 GAGATTAACTATCAATCACCGGCACAAAGAAGTAATGAAGGCGTCTCTTTTGGAAAACGT 155196
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growth regulator; animal feed product; thale cress;
cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
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ABL73975
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-DE-CGT02_1/USFTO spool/US10088187/runat_29122004_115842_107/app_query.fasta_1.519
-DB-N Geneseq_235ep04 - QFMT=fastap - SUFFIX=rng -MINNATCH=0.1 - LOOPCIX=0
-LOOPEXT=0 - UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORES-pct - THR MAX=100 - THR MIN=0 - ALIGN=15
-MODE=LOCAL - OUTFWT=pto - NORN=ext - HEAPSIXE=500 - MINLEN=0 - MAXLEN=20000000
-USRE=US10088187 @CGN 1 1 470 @runat_29122004 115442_107 - NCFU=6 - ICFU=3
-NO WMAP - LANGEQUERY - NEG SCORES=0 - WAIT - DSPELOCR=10 - LONGLOG
- DEV TIMEOUT=120 - WARN TIMEOUT=30 - THEADS=1 - XGARPEXT=0.5 - FGAPOP=6
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Altering plant characteristics, useful for producing plants for enzyme opharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
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Claim 1; SEQ ID NO 1817; 134pp; English

This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up characteristics. Specifically, it refers to identifying genes that are up care and an are as a constant of strong the heterodimeric EZFa/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, carey managentics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, blochemistry, signal corp. plants, altered hobidosynthesis, transduction, storage lipid mobilisation and/or altered photosynthesis, cach relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell wall biosynthesis, introgen and/or carbon metabolism or they function as transcription factors. This polymucleotide sequence is thale cress cDNA repressed 1.3 fold or more in plants overexpressing the EZPa/DPa

Sequence 1026 BP; 295 A; 235 C; 228 G; 268 T; 0 U; 0 Other;

ACAGTACCTGATGGTCATGTTTTGGCGTGTAGGACTAAGGAAAGCTGACAACAAAATTTGG rrrcaagargerrescaasacrrrerreaccerracrccarrcscarrestrarcrrrrs ArgieuPheGluAspleuGluAspGluAspAlaGluValIlePheProSerSerValTyr cerrrerrreaadacerreaadardaadardeceadgrearcrirerrerrerrerad ProSerProLeuProGluSerThrValProAlaAsnLysGlyTyrAlaSerSerAlaIle GluileAsnTyrHisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAla 1 AIGCCACGCCTTTCTTCCATAAGTTGATTTTCTCATCCACTATCCAAGAAAACGTCTG ArgValProAspLy8PheValSerLy8PheLy8AspGluLeuSerValAlaLeu ThrvalProAspGlyHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrp PheGlnAspGlyTrpGlnGluPheValAspArgTyrSerIleArglleGlyTyrLeuLeu MetProArgProPhePheHisLysLeullePheSerSerThr1leGlnGluLysArgLeu IlepheArgTyrGluGlyAsnSerAlaPheSerValTyrIlePheAsnLeuSerHisSer 1026 341 0 0 0 Length:
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161 GlnThrLeuPheThrGlyProValLysAlaGluGluProThrProThrProLysIlePro 180

960 321 GluLeuLeuArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyr 340 260 280 840 300 CTTGCGGAGAAACAATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGT 900 320 540 200 900 220 99 240 720 780 LeuproSerGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGln LeualaGluLysGlnTrpFroValArgCysLeuTyrLysAlaGlyArgAlaLysPheSer GlnGlyTrpTyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspValCysValPhe LyslysargGlyargLyslyslyssabnalaaspProGluGluIleAsnSerSeralaPro ArgAspAspAspProGluAsnArgSerLysPheTyrGluSerAlaSerAlaArgLysArg ThrValThrAlaGluGluArgGluArgAlaIleAsnAlaAlaLysThrPheGluProThr AsnProPhePheArgValValLeuArgProSerTyrLeuTyrArgGlyCysIleMetTyr VRN1; vernalisation; flowering; crop; Location/Qualifiers 269. .1294 /\*tag= a /product= "VRN1" BP A thaliana VRN1 coding sequence. AAF62446 standard; cDNA; 1495 BIOSCIENCE LTD 13-SEP-2000; 2000WO-GB003525 (first entry) Arabidopsis thaliana. WPI; 2001-273467/28. P-PSDB; AAB35491. Levy YY; GTC 1023 Val 341 WO200121822-A1 (PLAN-) PLANT 17-SEP-1999; 05-NOV-2001 29-MAR-2001. AAF62446; 1021 341 181 541 201 601 221 199 241 261 781 281 841 301 901 181 Dean C, RESULT 2 a 셤 셤 셤 ò 요 8 g ò 8 ò 셤 ⋧ 셤 à 용 ò ò

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                  1049 CTTCCTTCTGGGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAG
      ACCGTGACTGCAGAAGAAGAGAGAGAGCCATCAATGCAGCCAAAAACGTTCGAACCAACA
                                                                                                                                                                      CTTGCGGAGAAACAATGGCCTGTTCGATGTCTTACAAAGCCGGGAGAGCCAAATTCAGT
                                                                                                                                                                                                             GlnGlyTrpTyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspValCysValPhe
                                                                                                                                                                                                                                 CAAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTTT
                                                                                                                                                                                                                                                                        GluLeuLeuArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyr
                                                                                                                                                                                                                                                                                         1229 GAGCTGCTCAGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTAC
                                                                                           LeuProSerGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGln
                                                                                                                                                     LeuAlaGluLyaGlnTrpProValArgCysLeuTyrLyaAlaGlyArgAlaLyaPheSer
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                                                                                     The present invention provides the protein and coding sequences of Arabidopsis thaliana VRN1. This protein is capable of altering the vernalisation responses of a plant. Also provided are a number of PCR primers used to isolate the sequences. The sequences are useful in the production of crop plants, where they are able to control the timing of flowering, the duration of vernalisation required, the optimum temporature, or even eliminate the need for vernalisation completely. The present sequence is the VRN1 coding sequence
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Novel VRNI polynuclectide sequence encoding a polypeptide which alters vernalization response of plant in which VRNI nucleic acid is expressed, useful for influencing and assessing vernalization phenotype of plants.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                 Arabidopsis thaliana DNA fragment SEQ ID NO: 69076.
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300 rGlnGlyTrpTyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspValCysValPh 320
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                                        1184 TCAAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTGTTT
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                                                                                                                       ATGCCACGCCTTTCTTCCATAAGTTGATTTTCTCATCCACTATCCAAGAAAAACGTCTG
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                                                                                                                                                                                                                                                                      121 TTTCGATTTGATGTTCTCGCAATATTCTGTGCTGTTCTTATAGATATTGTGGACATTTAT
                                                                                                                                                                                                                                                                                                                                                                        PheValSerLysPheLysBapGluLeuSerValAlaValAlaLeuThrValProAspGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 CATGITIGGCGIGIAGGACTAAGGAAAGCIGACAACAAAATTIGGITICAAGAIGGIIGG
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 Local Similarity:
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3179 The present invention provides the protein and coding sequences of Arabidopsis thaliana VRNI. This protein is capable of altering the vernalisation responses of a plant. Also provided are a number of PCR primers used to isolate the sequences. The sequences are useful in the production of crop plants, where they are able to control the timing of Ilowering, the duration of vernalisation required, the optimum temperature, or even eliminate the need for vernalisation completely. The present sequence is the VRNI gene 9 Novel VRNI polynucleotide sequence encoding a polypeptide which alters vernalization response of plant in which VRNI nucleic acid is expressed, useful for influencing and assessing vernalization phenotype of plants. 3120 AGGGTCCCCAGATAAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTTGCTGTTGCACTC ThrValProAspGlyHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrp 21 ArgvalProAspLysPheValSerLysPheLysAspGluLeuSerValAlaValAlaLeu Sequence 5000 BP; 1447 A; 871 C; 931 G; 1750 T; 0 U; 1 Other; 5000 320 0 1 95 Length:
Matches:
Conservative:
Mismatches:
Indels:

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4260 TTCACTCTAGAGAACATTAGGAGAAGGAGGACGTCTGTGTGTTTGAGCTGCTCAGAACC 4319
                                                                                                                                     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                         326 ArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyrVal
                                                                                                                     Arabidopsis thaliana DNA fragment SEQ ID NO: 79593.
                                                                     AAC54934 standard; DNA; 1394 BP
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9905-0123180P.
9905-0125788P.
9905-0126768P.
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08-APR-1999;
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28-APR-1999;
30-APR-1999;
30-APR-1999;
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                                                                                                                                 3660 CCAGCTGAAGGCCAACGCCAACCCCAAAATACCTAAAAAGAGGAGGAGGAAGAAGAAA 3719
             ACAGTACCTGATGGTCATGTTTGRCGTGTAGGACTAAGGAAAGCTGACAAAATTTGG 3239
                                       3360 GAGATCAATTACCATTCCACGGTCTCATGGATTCCGCTCACAACCACTTCAAACGCGCC 3419
                                                                                                                                                                                                                                                    3600 TATCGCIGATTACGCGTCTTATCATTCTTTGAGGTTGATGCTTGATATTTTCCTTATCT 3659
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                                                              IlePheArgTyrGluGlyAsnSerAlaPheSerValTyrIlePheAsnLeuSerHisSer 100
                                                                                                GluileasnTyrHisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAla 120
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                            PheGlnAspGlyTrpGlnGluPheValAspArgTyrSerIleArgIleGlyTyrLeuLeu
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23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
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27-AUG-1999;
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28.8EP-1999
04.0CT-1999
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Pred. No.:
  99US-0139492P.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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21 ArgValProAspLysPheValSerLysPheLysAspGluLeuSerValAlaValAlaLeu 40

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21 ArgValProAspLysPheValSerLysPheLysAspGluLeuSerValAlaValAlaLeu 40

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PheGlnAspGlyTrpGlnGluPheValAspArgTyrSerIleArgIleGlyTyrLeuLeu 80

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                                                                                                                                                             621
                                       8SerGlulleAsnTyrHisSerThrGly-------beuMetAspSerAlaHisAs 115
                                                                         ePheProSerSerValTyrProSerProLeuProGluSerThrValProAlaAsnLysG1 154
                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                         aAlaLysThrPheGluProThrAsnProPhePheArgValValLeuArgProSerTyrLe
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                                                                nHisPhe---LysArgAlaArgLeuPheGluAspLeuGluAspGluAspAlaGluValII
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256 ITTCAAGACGGTTGGCAGGAGTTTGTCAACCGTTTCTCCATTCGGATTGGT------
             11epheArgTyrGluGlyAsnSerAlaPheSerValTyrilePheAsnLeu---Ser-Hi
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LeuProSerGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGln 280

Conservative: Mismatches: Indels: Gaps:

87.18% 81.20% 52.67%

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                GlnGlyTrpTyrGluPheThrLeuGluAenAsnLeuGlyGluGlyAspValCysValPhe 320
                                                                                               GluLeuLeuArgThrArgAspPhsValLeuLysValThrAlaPhsArgValAsnGluTyr 340
                                                                                                                                                    543
                                   LeuAlaGluLysGlnTrpProvalArgCysLeuTyrLysAlaGlyArgAlaLysPheSer 300
                                                          423
                                                                                                                                           Claim 144; SEQ ID NO 273; 577pp + Sequence Listing; English.
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an Arabidopsis thaliana nucleic acid (1). The polypeptide (II) encoded by (I), transgenic plant (III) or geneticallly condified cell (IV) are useful for screening a candidate agent for its biological effect, by combining the candidate agent with (II), (III) or (IV), and determining the effect of the candidate agent with (III) or (IV), and determining the modulate homologous or related genes, for congocial compositions that modulate the expression or function of its crocded protein, for mapping functional regions of the protein, in congocial passociated physiological pathways, for genetic manipulation of cells, preferantly plant cells, in screening assays of various plant strains to determine the strains that are capable of vichstanding a particular disease or environmental stress for enhancing or inhibiting production of blosynthetic product in a plant, for or inhibiting production of blosynthetic product in a plant, for or inhibiting production of blosynthetic product in a plant, for or inhibiting production of probes for the detection of mRNA in biological samples, to generate additional copies of (I), to generate ribozymes or oligonucleotides, and to create genetically modified and transgenic organisms, such as plant cells and plants. (II) or (III) is useful for introducing or improving disease resistance and stress consecution plants, for screening biological active agents, e.g., fundicides, insecticides, etc., and for elucidating biochemical pathways. (III) is useful as crops for their enhanced diseased resistance, enhanced clarates of interest, for screening programs, as crops which exhibit enhanced tolerance to environmental stress, or to produce a factor. This endance in plants a nucleic acid that may correspond to maturally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic organisms, such as plant cells and plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yu Y;
JP, Haas WD;
Hoffman N;
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Ledford BL, Woessner
Davis KR, Allen K,
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A, Mathew AV, L
er M, Slater T,
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HAMILTON C M.
PRICE J L.
RAINES T M.
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MATHEW A V.
LEDFORD B L.
WOESSNER J P.
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KRICKER M.
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RAMEAKA J G.
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Rameaka JG,
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(MATH/)
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                                                                                                                                                                                                                  GlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGlnLeuAlaGlu
                                                                                                                                                                                                                                                                                                               244 PheArgValValLeuArgProSerTyrLeuTyrArgGlyCysIleMetTyrLeuProSer
                                                                                                                                                                                365 GGGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAGNATGNGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 AGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTACGTC 132
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                                                                        Gaps:
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                                                                                                                                                                                     ---ValAlaLeuThrValProAspGlyHisValTrpArgValGlyLeuArgLysAlaAsp
                                                                                                                                                                                                                                                                                                                             97 LeußerHisSerGlu---IleAsnTyrHisSerThrGlyLeuMetAspSerAlaHisAsn
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0 U; 0 Other;
                                  1361
93
47
142
31
                                 Length:
Matches:
Conservative:
Mismatches:
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C; 371 G; 320
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 353 A; 317
                                    8.14e-21
298.50
44.73%
29.71%
16.62%
   Sequence 1361 BP;
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60 TrpPheGlnAspGlyTrpGlnGluPheValAspArgTyrSerIleArgIleGlyTyrLeu 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 LeuArgValproAspLysPheValSerLysPheLysAspGluLeuSerValAlaValAla 39
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58 ATTAGCATACCGGAGAAGTTGCGGACAGATTCAGTGGTCAGATCACCAAAGGGTTCAAC
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flower architecture and flowering time, useful in the area of
biotechnology, and commercial plant farming and agriculture.
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F, Kreps J, Provart N, Ricke
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                                                                                                                                                         Rice flowering time-related gene
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26-SEP-2001; 2001US-0325277P.
30-NOV-2001; 2001US-0334984P.
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293.50
45.43%
27.76%
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Glazebrook J, Katagiri
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20-MAY-1999;
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    96 AsnLeuSerHisSerGlu---IleAsnTyrHisSerThrGlyLeuMetAspSerAlaHis 114
                                                                                                                                                              ::: ||| || || || || 358 GGTCAGAATGCTGAGATACCATTTAAGTGATTCTGAAGATACTAGCACA--- 414
                                                                                                                                                                                                135 PheproSerSer---ValTyrProSerProLeuProGluSerThrValProAlaAsnLys 153
                                                                                                                                                                                                                         415 --- ccarcaacattrcragtregarcrccrcacaaggccrcracraagaaatrgaar 471
                                                                                                                                                                                                                                                   154 GlyTyrAlaSerSerAlaIleGlnThrLeuPheThrGlyProValLysAlaGluGluPro 173
                                                                                                                                                                                                                                                                    174 ThrProThrProLyglleProLysLysArgGlyArgLysLysLysAsnAlaAspProGlu 193
                                                                                                                                                                                                                                                                                                                            508 TTTTCAACAGGGAAGCCTGAAGATCCAAACAGCGGCGCTCTCATGTCAAACATGAG 567
                                                                                                                                                                                                                                                                                                                                                        194 GluileAsnSerSerAlaProArgAspAspAspProGlu------AsnArgSerLys 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 859 AAATACTACCATGCAAGCACTACCAGGGCTTCAATTGCCAACGCTGGATCAAGTTCATC 918
                                                                                                                                             115 AsnHisPhelysArgAlaArgLeuPheGluAspLeuGluAspGluAspAlaGluValIle 134
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AAC35159 standard; DNA; 796
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US-10-088-187A-11 (1-341) x AAC35159 (1-796)

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ò 셤 PhevalSerLysPheLysAspGluLeuSerValAlaValAlaLeuThrValProAspGly

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66.GlnGluPheValAspArgTyrSerIleArgIleGlyTyrLeuLeuIlePheArgTyrGlu 85

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	Length: Matches: Conservative: Mismatches: Indels: Gaps:
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126 LeuGluAspGluAspAlaGluValIlePheProSerSerValTyrProSerProLeuPro 145 :::	146 GluSerThrValProAlaAsnLysGlyTyrAlaSerSerAlaIleGlnThrLeuPheThr 165		166 GlyProValLyBAlaGluGluProThrProThrProLyBIleProLyBLyBArgGlyArg		186 LysLysLys-AsnAlaAspProGluGlulleAsnSerSerAlaProArgAspAspAs 204		204 pProGluAsnArgSerLysPheTyr	: : : : : : : : : : : : : : : : : : :	- E	617 GAAGAAGACAAGAGAGCCTCAGGGGATAACAGAGCTTTTAACAGAACCGAGACC 671	
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Search completed: December 30, 2004, 06:32:39 Job time : 581 secs

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Scoring table:

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Sequence 3, Application US/09351457
Setent No. 6312694
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APPLICANT: THORRE THILD E.
APPLICANT: RAN, SOPHIA
TITLE OF INVENTION: THAT BIND TO AMINOPHOSPHOLIPIDS
TITLE OF INVENTION: THAT BIND TO AMINOPHOSPHOLIPIDS
TITLE OF INVENTION: THAT BIND TO AMINOPHOSPHOLIPIDS
CURRENT APPLICANION NUMBER: US/09/351,457
CURRENT PILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 5
SOSTWARE: PALCHIN Ver. 2.0
SEQ ID NO 3
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Matches:
Conservative:
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TYPE: DNA
ORGANISM: Homo sapiens
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-351-543-3
US-09-561-526-3
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US-09-998-391-3
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US-08-119-386-3
US-08-418-595-5
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Database :

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Result

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Parent No. 634221
GRNERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
CURRENT FILING DATE: 2000-04-28
FRIOR APPLICATION NUMBER: US/09/561,108
CURRENT FILING DATE: 2000-04-28
FRIOR APPLICATION NUMBER: 60/131,432
FRIOR PILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOPTWARE: Patentin Ver. 2.0
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                                       US-10-088-187A-11 (1-341) x US-09-561-500-3 (1-2269)
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    1364 TGGAAAGAATATAAAGTGGGATTTGGTAACCCTTCAGGAGAATATTGGCTGGGAAATGAG 1423
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                                                                                                                             GluGlyAsnSerAlaPheSerValTyr---IlePheAsnLeuSerHisSerGluIleAsn 103
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APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTHONY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002500
CURRENT PEPLICATION NUMBER: US/09/561,500
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR PLILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VEY: 2.0
                                              ---IlePheArgTyr 84
                                                                                                                                                       104 Tyr-----HisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg
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Patent No. 6342219
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Patent No. 6406693
GENERAL INFORMATION:
APPLICANT: THORPE, PHILIP E.
APPLICANT: RAN, SOPHIA
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US-09-561-108-3
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TITLE OF INVENTION: CANCER TREATMENT METHODS USING ANTIBODIES TITLE OF INVENTION: AMINOPHOSPHOLIPIDS
FILE REFERENCE: 4001.002200
CURRENT APPLICATION NUMBER: US/09/351,543
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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1544 TATAGGATTCACCTTAAAGGACTTACAGGGACAGCCGGCAAAATAAGCAGCATCAGCCAA 1603
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pAspAspProGluAsnArgSerLysPheTyrGluSerAlaSerAlaArgLysArgThrVa 222
                                                                --- AlaAlaLysThrPh 237
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Sequence 3. Application US/09561499

Patent NO. 6524583

GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
TILE REPERBENCE: 4001.002582

CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR SEQ ID NOS: 44

SOFTWARE: PATENT VET. 2000-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PATENT VET. 2000-04-28
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                                                           Sequence 3, Application US/09561526

Batent No. 6416758

GRNERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002586
CURRENT APPLICATION NUMBER: US/09/561,526
CURRENT PILING DATE: 2000-04-28
RRIOR FILING DATE: 1099-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATCHING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 44
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SEQ ID NO 3
LENGTH: 2269
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Sequence 3, Application US/09561005
Sequence 3, Application US/09561005
Patent No. 6703020
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rolf A. Brekken
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE METHODS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002585
CURRENT FILING DATE: 2000-04-28
FRICH APPLICATION NUMBER: 60/131,432
FRICH FILING DATE: 1999-04-28
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|1724 TACTATCCACAGAGGCAGAACACAAATAAGTTCAACGGCATTAAATGGTACTACTGGAAA 1783
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1724 TACTATCCACAGAGGCAGAACACAAATAAGTTCAACGGCATTAAATGGTACTACTGGAAA 1783
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| GCTCAGGCTATTCGCTCAAGCCACAACCATGATGATCCGACCAGCAGATT-----
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| Sequence 3, Application US/0999831
| Patent No. 667641
| GENERAL INFORMATION:
| APPLICANT: Philip E. Thorpe
| APPLICANT: Philip E. Thorpe
| TITLE OF INVENTION: INHIBITING VEGP
| TITLE OF INVENTION: INHIBITING VEGP
| FILE REFERENCE: 4001.002584
| CURRENT APPLICATION NUMBER: US/09/998,831
| CURRENT FILIG DATE: 2001-11-30
| PRIOR FILIG DATE: 2001-04-28
| NUMBER OF SEQ ID NOS: 44
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 3
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                                    167 oValLysAlaGluGluProThrProThrPro-
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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    ||||||| ::: ::: ::: ::: ||||::||| | TTIGITITCGCAACCTAAACAGACTGG 1483
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                                                                                                                                              138 SerValTyr-----ProGluSe 147
                                                                                                                                                                                  147 rThrValProAlaAsnLysGlyTyrAlaSerSerAlaIleGlnThrLeuPheThrGlyPr 167
                                GluGlyAsnSerAlaPheSerValTyr---IlePheAsnLeuSerHisSerGluIleAsn 103
                                                                    104 Tyr-----HisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg 121
                                                                                                        122 LeuPheGluhspLeuGluhspGluhspAlaGlu------ValIlePheProSer 137
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45 GIYHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrpPheGlnAspGly
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APPLICANT: Davis, et al.
TITLE OF INVENTION: THE-2 LIGAND, METHOD OF MAKING AND USES TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: Requeron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STRTE: New York
COUNTRY: USA
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                                                                                                                                                                                               167 oValLysAlaGluGluProThrProThrPro----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 5, Application US/08418595 ; Patent No. 5814464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1893 CTTAAGCCCAGTGCAC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1992 AGAGCCTGTAAAC 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 eGluProThrAsn 241
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US-08-418-595-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1371 İĞGAAAGAATATAAAGTGGGATTTGGTAACCCTTCAGGAGAATATTGGCTGGGAAATGAG 1430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluGlyAsnSerAlaPheSerValTyr --- IlePheAsnLeuSerHisSerGluIleAsn 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 Tyr-----HisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 GlyHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrpPheGlnAspGly 64
YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
REGISTRATION NUMBER: 36,108
REERENCE/DOCKET NUMBER: REG 330-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 345-7400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,261
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,932
FILING DATE: 07-OCT-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                       FILING DATE: 17-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/353,503
FILING DATE: 09-DEC-1994
PRIOR APPLICATION DATA:
                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,579
FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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37.55%
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STRANDEDNESS: single
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Best Local Similarity:
Query Match:
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US-08-373-579-5
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Pred. No.:
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1932 GTCCTCTTCCACCACAGAGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCAGATT 1991
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|11| CCAGGAAATGATTTTAGCACAAAGGATGGAGACACAACGACAAATGTTTGCAAATGTTCA 1670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 rThrValProAlaAsnLysGlyTyrAlaSerSerAlaIleGlnThrLeuPheThrGlyPr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 oValLysAlaGluGluProThrProThrPro------LysileProLysLy 182
                                                                                                                                                                                                                                                                                                                                                                                                                                           GluGlyAsnSerAlaPheSerValTyr---IlePheAsnLeuSerHisSerGluIleAsn 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tyr-----HisserThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg 121
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                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2282 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
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|1992 AGAGCCTGTAAAC 2004
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5.79%
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Best Local Similarity:
Query Match:
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; LOCATION:
US-08-418-595-5
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GluGlyAsnSerAlaPheSerValTyr---IlePheAsnLeuSerHisSerGluIleAsn 103
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                                               GENERAL INFORMATION:
APPLICANT: Valenzuela et al.
APPLICANT: Valenzuela et al.
TITLE OF INVENTION: TIB LIGAND-3, METHODS OF MAKING AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reqeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2282
58
34
92
61
                                                                                                                                                                                                                                                                                     COMPUTER: REPORT disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,926
FILING DATE: 19-JUN 1996
CLASSIFICATION: 435
ATTONREY/AGBAT INPORMATION:
NAME: RODERT J. CODERT
REGISTRATION NUMBER: 36,108
REPRENCE/POCKET NUMBER: 36,108
REPRENCE/POCKET NUMBER: 36,108
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2282 base pairs
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-088-187A-11 (1-341) x US-08-665-926-5 (1-2282)
US-08-665-926-5; Sequence 5, Application US/08665926; Patent No. 5851797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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37.55%
23.67%
5.79%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
357..1847
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                 CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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1311 GGAGGCGGGTGGACAATTATTCAGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGGACT 1370
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|TTGTTTCGCAACTGACTAATCAGCAACGCTATGTGCTTAAAATACACCTTAAAGACTGG 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1843 -----TCTAAACATCCCAGTCCACCTGAGGAACTGTCTCGAACTATTTCAAAGA 1892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 Tyr-----HisSerThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuPheGluAspLeuGluAspGluAspAlaGlu------ValllePheProSer 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 SerValTyr------ProGluSe 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyHisValTrpArgValGlyLeuArgLysAlaAspAsnLysIleTrpPheGlnAspGly 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 PheValAspArgTyrSerIleArgIleGlyTyrLeuLeu-----IlePheArgTyr
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58
34
92
61
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   indels:
                                                                                                      330-D
US 08/319,932
             FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Cobert, Robert J.
REGISTRATION NUMBER: 36,108
                                                                                               REFERENCE/DOCKET NUMBER: R
TELECOMMUNICATION INFORMATION
TELEPHONE: (914) 345-7400
                                                                                                                                         TELEPHONE: (914) 345-7400
TELEPAX: (914) 345-7721
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 2282 base pairs
                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104.00
37.55%
23.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.79%
                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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357..1847
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 TrpGln----
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                   US-09-162-437-5
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                                                      1611 CCAGGAAATGATTTTAGCACAAAGGATGGAGACAAACGACAAATGTATTTGCAAATGTTCA 1670
                                                                                                                                         1671 CAAATGCTAACAGGAGGCTGGTGTTTGATGCATGTGGTCCTTCCAACTTGAACGGAATG 1730
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|1731 TACTATCCACAGAGGCAGAACACAAATAAGTTCAACGGCATTAAATGGTACTACTGGAAA 1790
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                                                                                                                                                                                                                                                                       --LysileProLysLy 182
                                                                                                                                                                                                                                                                                                                                                                                                                                      pAspAspProGluAsnArgSerLysPheTyrGluSerAlaSerAlaArgLysArgThrVa 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 lThrAlaGluGluArgGluArgAlaIleAsn------AlaAlaLysThrPh 237
                                                                                                                                                                                                                                                                                                            1791 GGCTCAGGCTATTCGCTCAAGGCCACAACCATGATGATCGACCAGCAGATT-----
                   -----ValllePheProSer
                                                                                                                                                                                                                                                                                                                                                      182 sArgGlyArgLysLysLysAsnAlaAspProGluGluIleAsnSerSerAlaProArgAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT:
Davis, et al.
TILLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reqeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
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               122 LeuPheGluAspLeuGluAspGluAspAlaGlu--
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PILING DATE: 17-7AN-1995
RILING DATE: 09-DEC-1994
PRICATION NUMBER: US 08/348,492
APPLICATION NUMBER: US 08/348,492
FILING DATE: 02-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/30,261
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/373,579
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10591
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/418,595
FILING DATE: 06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09162437
Patent No. 6166185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTAAGCCCAGTGCAC---
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                                                                                               138 SerValTyr-
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1992 AGAGCCTGTAAAC 2004
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US-08-817-318-5
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                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Davis, et al.

TITLE OF INVENTION: Expressed Ligand - Vascular

TITLE OF INVENTION: Intercellular Signalling Molecule
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Regeneron Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Human TIB-2 ligand 2
LOCATION: 1...2282
OTHER INFORMATION: from clone pBluescript KS
OTHER INFORMATION: encoding human TIE 2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
Indels:
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                               lThrAlaGluGluArgGluArgAlaIleAsn----
                                                                                                                                                                                                                                                                                                    E: Regeneron Pharmaceuticals, Inc 777 Old Saw Mill Road
.893 CTTAAGCCCAGTGCAC------
                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: CODERT, ROBERT J
REGISTRATION NUMBER: 36,108
REFERENCE/DOCKET NUMBER: REG 333
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEPAK: 914-345-7721
INPOREMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            Sequence 5, Application US/08740223A Patent No. 6265564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Coding Sequence
LOCATION: 357...1844
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                     1992 AGAGCCTGTAAAC 2004
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TYPE: nucleic acid
STRANDEDNESS: single
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104.00
37.55%
23.67%
5.79%
                                                                                          237 eGluProThrAgn 241
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                  STREET: 777 Old :
CITY: Tarrytown
STATE: NY
COUNTRY: USA
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Best Local Similarity:
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Query Match:
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1791 GGCTCAGGCTATTCGCTCAAGGCCACAACCATGATGATCCGACCAGCAGATT----- 1842
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| 1731 TACTATCCACAGAGGGAGAACACAAATAAGTTCAACGGCATTAAATGGTACTACTGGAAA 1790
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1932 GTCCTCTTCCACCACAGAGGGGTGTGCTGGTGCTGACGGGACCCACATGCTCCAGATT 1991
                                                                                                                                                                                                                                                                                                                                                                                                              1371 TGGAAAGAATATAAAGTGGGATTTGGTAACCCTTCAGGAGAATATTGGCTGGGAAATGAG 1430
                                                                                                                                                                                                                                                                                                           167 oValLysAlaGluGluProThrProThrPro-------LysileProLysLy 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 sArgGlyArgLysLysLysLasnAlaAspProGluGluIleAsnSerSerAlaProArgAs 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 LeuPheGluAspLeuGluAspGluAspAlaGlu------ValIlePheProSer 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---- ProSerProLeu-ProGluSe 147
                                                                                                                                                                           84
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                                                                                                                                                                             -----IlePheArgTyr
                                                                                                                                                                                                                                                                           GluGlyAsnSerAlaPheSerValTyr---IlePheAsnLeuSerHisSerGluIleAsn
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TITLE OF INVENTION: TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF FILE REFERENCE: REG 330-F-PCT-US
CURRENT APPLICATION NUMBER: US/08/817,318
CURRENT FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PASTSEQ for Windows Version 3.0
SEQ ID NO 5:
LENGTH: 2282
                                                                                                                                                                           Pheval AspArgTyrSerIleArgIleGlyTyrLeuLeu-
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COTHER INFORMATION: Unknown Organism
NAME/KEY: CDS
LOCATION: (357)...(1847)
US-08-817-318-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5, Application US/08817318 ; Patent No. 6433143
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1371 TGGAAAGAATATAAAGTGGGATTTGGTAACCCTTCAGGAGAATATTGGCTGGGAAATGAG 1430
                                                                                                                                                                                                                                                                                                                   1551 TATAGGATTCACCTTAAAGGACTTACAGGGACAGCCGGCAAAATAAGCAGCATCAGCCAA 1610
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1731 TACTATCCACAGAGGCAGAACACAAATAAGTTCAACGGCATTAAATGGTACTACTGGAAA 1790
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Search completed: December 30, 2004, 09:53:17 Job time: 227 secs

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Sequence 237, App Sequence 1320, Ap Sequence 1320, Ap Sequence 3743, Ap Sequence 89685, A Sequence 89631, A Sequence 89631, A Sequence 22044, A

Sequence 3743, Sequence 89685 Sequence 89631 Sequence 32044 Sequence 75700 Sequence 75700

Sequence 107372, Sequence 101386, Sequence 49771, A

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Searched:

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Sequence 2973, Ap

Sequence 75700, A Sequence 23571, A Sequence 7926, Ap

Sequence 1316, Ap Sequence 97592, A Sequence 1317, Ap Sequence 9015, Ap

Sequence 273, App Sequence 118105, Sequence 1318, Ap

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Sequence 1318, Application US/10767795

Publication No. US2004018130A1

GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Jou, Yihua
APPLICANT: Jou, Yihua
APPLICANT: Jou, Yihua
APPLICANT: Jou, Yihua
APPLICANT: Jou, Yihua
APPLICANT: Jou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53534)B
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NOS: 117596
                                                                     08-09-938-842A-273
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08-10-424-599-118105
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-Q=/cgn2 1/USPTO spool/US1008 NA -QFMT=fastap -SUPFTIX=xnpb -MINARTCH=0.1
-LCOPCLI 0 -LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pto -NORM=ext -HEARSTZE=500 -MINLEN=0
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :

Sequence 2973, Application of the property of

Sequence 312, App Sequence 89684, A

; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C1540\_1 US-10-767-795-1318

SUMMARIES

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ArgserlysphetyrGluserAlaserAlaArgLysArgThrValThrAlaGluGluArg 227
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Sequence 273, Application US/09938842A

Sequence 273, Application US/09938842A

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Sequence 273, Application US/09938842A

Sequence 273, Application US/09938842A

APPLICANT: Harper, Jeff

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPI30-3

CURRENT APPLICATION NUMBER: US 60/227, 866

PRIOR FILING DATE: 2000-08-24

PRIOR PILING DATE: 2001-01-16

PRIOR PLING DATE: 2001-01-16

PRIOR PLING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 273

LENGTH: 681
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Sequence 118105, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION: UNDER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 18105
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  GAACCAGTGAATAAAGGTTATGGCGGTTCTACAGCCATCCAAAGCTTTTTCAAA---GAA 165
                                                           166 TCTAAAGCTGAAGAA-----ACGCCCAAGGTACTTAAGAAGAAGAAGAAGAAGAAG 216
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Query Match:
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| Sequence 273, Application US/09938842A
| Publication No. US20040009476A9
| GENERAL INFORMATION:
| APPLICANT: Harper, Joef
| APPLICANT: Kreps, Joel
| APPLICANT: Kreps, Joel
| APPLICANT: Wang, Xun
| APPLICANT: Wang, Xun
| APPLICANT: Wang, Xun
| APPLICANT: Wang, Xun
| APPLICANT: Wang, Ann METHODS OF USE
| TITLE OF INVENTION: SAME, AND METHODS OF USE
| FILE REFERENCE: SCRIP1300-3
| CURRENT FILING DATE: 2001-08-24
| PRIOR APPLICATION NUMBER: US 60/227,866
| PRIOR APPLICATION NUMBER: US 60/264,647
| PRIOR APPLICATION NUMBER: US 60/300,111
| PRIOR PILING DATE: 2001-01-16
| PRIOR PILING DATE: 2001-01-16
| PRIOR PILING DATE: 2001-06-22
| NUMBER OF SEQ ID NOS: 5379
| SEQ ID NO 273
| LENGTH: 681
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  277 CGCTCAAAGTTCTACGAGAGTGCTTCTGCTAGAAAGAGAACTGTAACTGCAGAGGAAAGA 336
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                                       GTGAGGTGCCTCTACAAAGCAGGGAGAGGCTAAGTTTAGCCAAGGATGGTTGAGTTCACA
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US-09-938-842A-273
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812 TGTCTTAAATTTTTGAAGAAATGGAAGGTGAAGATTCCATTGAAATCTCGGATTCATCA 871
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Sequence 1316, Application US/10767795
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; Publication No. US20040181830A1
; GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 38-21(53534)B
; CURRENT PEDLICATION NUMBER: US/10/767,795
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 117596
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TTCTGCGTCTAAAGTTAATAACTGCATGAACTGGAGTGATGAAATCAATTTTTCGTGCGTT
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US-10-767-795-1316
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Matches:
Conservative:
Mismatches:
Indels:
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880.00
67.81%
57.50%
49.00%
                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Gossypium hirsutum
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Best Local Similarity:
                                                                    RESULT 5
US-10-767-795-1316
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DB:
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60 pPheGlnAspGlyTrpGlnGluPheValAspArgTyrSerIleArgIleGlyTyrLeuLe 80 	80 ullePheArgTyrGluGlyAgnSerAlaPheSerValTyrIlePheAgnLeuSerHigSe 100	100 rGlulleAsnTyrHisSerThr	114   SASHHISPNELYSArgAlaArgLeuPheGluAspLeuGluAspGluAspAla	132 -GluValIlePheProSerSerValTyrProSerProLeuProGluSer 147	148ThrValProAla	152 160 	161	-ProVallyshaduGluGluProThrProThrProLy	178 sIleProLysLysRagGlyArgLysLysLysRasnAlaAspProGluGluIleAsnSerSe 198	198 ralaProArgAspAspProGluAsnArgSerLysPheTyrGluSerAlaAr 218	218 glygargThrValThrAlaGluGluArgGluArgAlaIleAsnAlaAlaLysThrPheGl 238 	238 uProThrAsnProPhePheArgValValLeuArgProSerTyrLeuTyrArgGlyCys11 258	258 eMetTyrLeuProSerGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLy 278	278 sValginLeuAlagluLysGinTrpProValArgCysLeuTyrLysAlaglyArgAl 297	297 aLysPheSerGlnGlyTrpTyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspVa 317 	317 1CygValPheGluLeuLeuArgThrArgAspPheValLeuLygValThrAlaPheArgVa 337	Oy 337 lAsnGlu 339  Db 1358 AACCGAG 1364  RESULT 7
oy Op	S a	ራ ብ	<u>ኞ</u>	<i>장</i> 옵	& A	& €	<i>8</i> €	o da	& A	& A	<i>አ</i> ን ብ	<b>중</b> 옵	<i>ት</i>	\$ A	& &	& g	RE DO CY
Qy 172 uProThrProThrProLys1leProLysLysArgGlyArgLysLysAsnAlaAspPr 192 	Qy 192 ogludlulleasnSerSeralaProArgAspAspAspProGluAsnArgSerLysPheTy 212	Qy 212 rGluseralaseralaatgUysArgThrValThralaGluGluArgGluArgAlaIleAs 232 	Qy 232 nAlaAlaLysThrPheGluProThrAsnProPhePheArgValValLeuArgProSerTy 252 	Oy 252 rLeuTyrArgGlyCygIleMetTyrLeuProSerGlyPheAlaGluLygTyrLeuSerGl 272 	QY       272 ylleSerGlyPhelleLygValGlnLeuAlaGluLygGlnTrpProValArgCygLe       291         Db       992 GGTTTCGGGATTTATTAAACTTCAGCTTCCAGATGGGACAATGGCCCGTTCGATGTCG       1051	Oy 291 uTyrLysAlaGlyArgAlaLysPheSerGlnGlyTrpTyrGluPheThrLeuGluAsn 310    :::	RESULT 6 US-10-424-599-97592 ; Sequence 97592, Application US/10424599	0	<ul> <li>APPLICANT: Zhou Yihua</li> <li>FAPLICANT: Cao Yongwei</li> <li>TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With</li> <li>TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement</li> </ul>	; FILE REFERENCE: 38-4153-43-15 ; CURRENT APPLICATION NUMBER: US/10/424,599 ; CURRENT FILING DATE: 2003-04-28 ; NUMBER OF SEQ ID NOS: 285684	; SEQ IN 0 9/592 ; LENGTH 1760 ; TYPE: DNA ; ORGANISM: Glycine max	; FEATURE: ; OTHER INFORMATION: Clone ID: PAT_MRT3847_59139C.1 US-10-424-599-97592	1.43e-95 Length: 835.50 Matches: 58.81\$ Conservative:	••	-10-088-187A-11 (1-341) x US-10-424-599-97592 (1-1760)  1 MetProArgProPhePheHisLysLeullePheSerSer-ThrileGlnGluLysArgLe	DD 182 AIGCCTIGITICCICAAGCTIGCTACATCCTCATCTACATACCTGATACT 241  Qy 20 uArgValProAspLysPheValSerLysPheLysAspGluLeuSerValAlaValAlaLe 40  Qy 20 QACGATACTATACTACTACTACTACTACTACTACTACTACTACT	242 40 302

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5.57e-64
582.50
60.96%
52.19%
                                                                                                                                   TYPE: DNA
ORGANISM: Gossypium hirsutum
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Best Local Similarity:
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US-10-021-323-9015
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Sequence 1317. Application US/10767795
Sequence 1317. Application US/10767795
Publication No. US20040181830A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihue
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 1317
LENGTH: 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 GAAGAAAGAGAGAGGAATCAATGCGGCCAAAGCATTTGAGCCTACTAACCCTTTCTGC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgValValLeuArgProSerTyrLeuTyrArgGlyCysIleMetTyrLeuProSerGly 264
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                                                                                                                                                                                                                                                                                                                                                                                        185 ArglyslyslyskanalaAspProGluGlulleAsnSerSerAlaProArgAspAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                     165 ThrGlyProValLysAlaGluGluProThrProThrProLysIleProLysLysArgGly
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                                                                                                                                                                                             OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C1540_2
                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
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Matches:
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US-10-021-323-9015
; Sequence 9015, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
                                                                                                                                                                                                                                                                                                                                                                    141 TCAGGTGCTATGAAACCAGAA----
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640.00
82.49%
74.01%
35.63%
                                                                                                                                                                         ORGANISM: Gossypium hirsutum
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Query Match:
DB:
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131
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LOCATION: (1)..(644)
OTHER INPORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3828-022-Q1-K6-E11
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Mismatches:
Indels:
APPLICANT: Feng, Paul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Ziegler, Todd E.
TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)8
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 17880
| LENGTH: 644
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Sequence 97591, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Acvalic David K

APPLICANT: Acvalic David K

APPLICANT: Acvalic David K

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

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                                                                                                                TyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspValCysValPheGluLeuLeu
                                                                                                                                                                                                                324 ArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyrVal 341
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Matches:
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_59138C.1
US-10-424-599-97591
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US-10-767-795-1320
Sequence 1320, Application US/10767795
; Publication No. US20040181830A1
; GENERAL INFORMATION:
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Best Local Similarity:
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                          aAlaLysThrPheGluProThrAsnProPhePheArgValValLeuArgProSerTyrLe
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APPLICANT: Garcia, Carlos A.
APPLICANT: Stader, Maja
APPLICANT: Davier, Ted
APPLICANT: Davier, Ted
APPLICANT: Davier, Ted
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Ltalian
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: LABLIANA
TITLE OF INVENTION: LABLIANA
TITLE OF INVENTION: LABLIANA
TITLE REFERENCE: 2028 (PARA-017RV)
CURRENT APPLICATION NUMBER: US/09/770,423
CURRENT APPLICATION NUMBER: 60/178,512
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 237
LENGTH: 426
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                                                                                                                                                                                                                                           604 ATACCGGGGATGTATTATGTACTTACCATCA 634
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Publication No. US20020040490A1
GRBERAL INFORMATION:
APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jemnifer L.
APPLICANT: Raines, Tracy M.
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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COCATION: (1)...(426)
COTHER INFORMATION: n = A.T.C or
US-09-770-423-237
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Rameaka, Joshua G.
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Best Local Similarity:
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US-09-770-423-237/c
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Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihue
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
SEQ ID NO 1120
LENGTH: 650
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Indels:
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, OTHER INFORMATION: Clone ID: LIB3543-054-Q1-K6-E2
US-10-767-795-1320
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54.82%
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                                                                                                                                      TYPE: DNA ORGANISM: Gossypium hirsutum
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Best Local Similarity:
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US-10-739-930-3743/c
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1367 AAGAGAAAAGTTAACTCCAGTTGAATTTCTTCAACAATGTCAAATGAGAAGTCGCAAGTGT 1308
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                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                              LOCATION: (1)..(2207)
OTHER INFORMATION: unsure at all n locations
CURRENT FILING DATE: 2003-12-18
WHDER OF SEQ ID NOS: 11088
SEQ ID NO 3743
LENGTH: 2207
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329.00
43.77%
27.25%
18.32%
                                                                                                                                            (2207)
                                                                      TYPE: DNA
ORGANISM: Glycine m
PEATURE:
NAME/KEY: unsure
LOCATION: (1)..(220
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Best Local Similarity:
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1451 AATCCCACCTTCAGTTTGTTAGACGAATCCAAGACTTTCAACAAGACTCAGATCAGAGAC 1510
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TCCCAAAGGCGCCGAGTAACCGAAGAAGAGAAGTGCCTTGCTCTCAGAAAGGCAATGGAG 1630
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                                                  100 SerGlulleAsnTyrHisSerThrGlyLeuMetAspSerAla--------
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                                                                                                                114 ---HisAsnHisPheLysArgAlaArgLeuPheGlu-
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; Publication No. US20040123343A1
; RENERAL INFORMATION:
; APPLICANT: LA ROBA, Thomas J.
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Publication No. US20040214272A1
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
APPLICANT: Cao, Yongua
APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
 1127 GGTAGTCTGAACTTACCAATGAAGTTCTGAAGAGTCACCTTGATTTGCACAAGAAGCGG 1068
                                                                                                              GlyPheileLysValGin---LeuAlaGluLysGlnTrpProValArgCys---LeuTyr 292
                                              257 CyslleMetTyrLeuProSerGlyPheAlaGluLysTyrLeuSer-----GlylleSer 274
                                                                                                                                                                                LysAlaGlyArgAla---LysPheSerGlnGlyTrpTyrGluPheThrLeuGluAsnAsn 311
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318 ACCATGTTCAACCAGCACCTCAAGGAGCAGCCAACCGGAGCAGTTTCCCTGAGAGGC 877
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Query Match:
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US-10-425-115-89685
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LENGTH: 2338
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 32044
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778 GTGTCTCGGCGTGGTAGATGTTTTCAAAGGGTCAAAGACAACTAACAGTAATATCACAG 719
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                                      196 AsnSerSerAlaProArgAspAspAspProGluAsnArgSerLysPheTyrGluSerAla
                                                                     LysargThrValThrAlaGluGluArgGluArgAlaIleAsnAlaAlaLysThrPheGlu
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Matches:
Conservative:
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                                                                                                                216 SerAlaArg-----
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ORGANISM: Zea mays
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                                                                         APPLICANT: Wu, wu, Andrey A. APPLICANT: Boukharov, Andrey A. APPLICANT: Buckharov, Brad APPLICANT: Buckharov, Brad APPLICANT: Li, Pint. Buck Trit. Di, Pint. Brack Trit. Di, Pint. Brack Trit. Brack Trit. Dr. INVENTION: Plants and Uses Thereof for Plant Improvement FILLE REPRENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 89631 LENGTH: 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTGACAAGATATCAACT-----TTCTCTGCTCACCCT-----TCCAAAATGTG 1118
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           Kovalic, David K
Zhou, Yihua
Cao, Yongwei
Wu, Wei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    876 GCTGATCATCTTGGGGAAAGAGCGCACAACATCATACTTCGTAGGCCGAACAGGAGGAG 935
                                                                               237 CACCTGAAATCACCTAGCAGCGCTGAGACATGGCACGTCGGTGTAGAGAAGCATGGCGAC 296
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                                                    39 AlaLeuThrValPro---AspGlyHisValTrpArgValGlyLeuArgLysAlaAspAsn 57
ArgLeuArgValProAspLysPheValSerLysPheLysAspGluLeuSerValAlaVal 38
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1 (bases 1 to 1307)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana (thale cress)
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(c) 1993 - 2004 Compugen Ltd
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Database :

Š. Result

HTC 06-FEB-2004

from clone

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BX823300.1 GI:42464860

HTC; GSLT_CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1441)

S Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,

Menard,M., Craudd,C., Quetier,F., Scarpelli,C., Schachter,V.,

Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.

Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
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Life Technologies (a division of Invitrogen) members carried out full-length libraries construction. Temple G.

Genoscope members carried out sequencing and annotation. Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein http://www.genoscope.cns.ff/externe/sequences/Banque_Projet_EF/Full
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS20ZG12 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage BP 191 91006 ENRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                       ACCGTGACTGCAGAAGAAGAAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCAACA
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Location/Qualifiers
    CGAGATGATCACAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGA
                                                                                                                               AsnProPhePheArgValValLeuArgProSerTyrLeuTyrArgGlyCysIleMetTyr
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                                             ThrValThrAlaGluGluArgGluArgAlaIleAsnAlaAlaLysThrPheGluProThr
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Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Wunich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
                                                                                                                                     http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
Location/Qualifiers
1. 1307
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/clone="GSLTFB502E05"
/tissue type="Rlowers and bu
/plasmid="pcMvSPORT 6"
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/gene="At3g18990"
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Arabidopsis thaliana Full-length CDNA Complete sequence from clone GSLTFGRF4Z804 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).

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Arabidopsis thaliana (thale cress).

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; Cosids; to 1375)

Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M. Whole Genome Sequence Comparisons and 'Pull-Length' cDNA Sequences:
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Direct Submission
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web. : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (advision of Invitrogen) members carried out
full-length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jailno O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clept C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
Genome released by MIPS (Munich Information center for Protein
Sequences). S prime and 3 prime are assembled with Phrap.
Lingt/www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
Lingt/
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      LeuProSerGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGln
                                            1011 crirccrircreserriscresasascraccrascresearcresescrearcasascress
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/tissue type="Adult vegetative tissue"
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complement(1. .1441)
/gene="At3g18990"
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Direct Submission

Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (adivision of Invitrogen) members carried out

full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli

V., Aury J.M., Jaillan O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clept C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis Annotation is based on the June 2003 version center for Protein Sequences) 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full

Lengt,
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BX816536
BX816536
BX816536
BX816536.1 GI:42473594
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 1346)
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M. Wole Genome Sequence Comparisons and 'Full-Length' CDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                CNSOADSP 1346 bp mRNA linear HTC 06-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH54ZB06 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
                                           1125 CAAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTGTCT 1184
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Location/Qualifiers
                              321 GluLeuLeuArgThrArgAspPheValLeuLysValThrAlaPheArgValAsnGluTyr
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Matches:
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2 (bases 1 to 1346)
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RESULT 5 CNSOAD32 LOCUS LOCUS LOCUS LOCUS DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH452CO5 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).  ACCESSION BASH6391. BKB16391.	Temple, G., Caboche, M., Weissenbach, J. and Salancubat, M.  TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation JOURNAL Unpublished REFERENCE 2 (bases 1 to 1420) AUTHORS Genoscope.  TITLE Direct Submission JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr) COMMENT The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Wenard M., Cruaud C.,	Schachter V., Weissenbach J., Salanoubat M.  URGY INRA: Clepter C., Caboche M.  Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.  http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.  Location/Qualifiers  Location/Qualifiers  1. 1420 / organism="Arabidopsis thaliana" / mol_type="mRNA" / source / sequences/arabidopsis. / clone=GSLTPEHEMA" / stain="Col-0" / tssue type="mRNA" / tissue type="Hornon-Treated Callus"		US-10-088-187A-11 (1-341) x CNSOAD3Z (1-1420)  Qy
Met ProArgProPhePheHisLysLeullePheSerSerThrileGlnGluLysArgLeu	IlePheArgTyrGluGlyAsnSerAlaPheSerValTyrIlePheAsnLeuSer-Hi  TTCAGATACAAGTTACAGTCTACATTTTCAATTTTCCCCCAGA  TTCAGATACAA	154 YFyrAlaSerSerAlaIleGInThrLeuPheThrGIyProValLysAlaGluGluPr 173	233 aAlaLysThrPheGluProThrAsnProPhePheArgValValLeuArgProSerTyrLe 253 745 AGCCAAAACATCGAAATCCTTAGAGTTGTTCTGCGACCATCATATTTTTTTT	

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Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
Bp 191 91006 ENVEX cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.

Infe Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.
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WRGY INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 1490)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Craudd,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPCH13ZB06 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).

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                                                                      PheGlnAspGlyTrpGlnGluPheValAspArgTyrSerIleArgIleGlyTyrLeuLeu 80
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                                                                                             CGCCTTTCGTGTCAATGAGTATGTG 1176
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CK120978 GI:47831294
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Arabidopsis thaliana
Brukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 780)
Peilner, Tr., Immink, R.G.H., Cahill, D.J. and Kersten, B.
Generation of a cDNA expression library from Arabidopsis
inflorescence meristem
Unpublished (2003)
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rala-GluGluargGluargalaIleasnAlaAlaLysThrPheGluProThrAsnProP 243
                                                           pAspProGluAsnArgSerLysPheTyrGluSerAlaSerAlaArgLysArgThrValTh 223
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Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Innestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131648
Fax: +49(0)30/8413128
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/organism="Arabidopsis thaliana"
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Insert Length: 780 Std Error:
Plate: 204 row: O column: 14
Seq primer: pOE65
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using SuperscriptTM-system (Invitrogen) with an oligo (dT)-primer containing NotI restriction site and a SalI adapter. The main library (plate numbers begin with 1) of 38,000 clones was rearrayed into the sublibrary (plate numbers begin with 201) containing 5,000 putative expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABJ-LAPP; data are also accessible at https://gabi.rzpd.de"
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ORIGIN		4-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1		
Alignment S Pred. No.: Score: Percent Sim Best Local Query Match	Scores: .milarity: .Similarity: .h:	1.12e-98 1016.50 83.09\$ 75.90\$ 56.60\$	Length: Matches: Conservative: Mismatches: Indels: Gaps:	780 211 20 21 26 9
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ò	54 LysAlaAspA:	AsnLysileTrpPh	eG1nAspG1yTrpG1n(	GluPheValAspArgTyrSer 73
g G	2 AAAGCCAAC	AACAAAATCTGGTT	rcaadacddrrddcad	aaccettr
δ	74 IleArglle	eGlyTyrLeuLeuIlo	ePheArgTy	rGluGlyAsnSerAlaPheSerValTyr 93
Dp	62 ATTCGGATTGGT	GGT	-TTCAGATACAA	Grracacrcrac 97
Š	94 IlePheAsnL	LeuSer-HisS	erGlulleAsnTyrHi	sserThrGly 108
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δλ	109 -LeuMetAspS	spSerAlaHisAsnHi	sPheLysArgAl	aArgLeuPheGluAspLeuGl 127
Dp	158 GCAAATGGATTC	ATTCCGCACAGAATC	agticaacaaacgigc	ATTO
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qa	218 ACTCAAAG	ACTCAAAGATGCTAAGGTCATTTATCCATCGAAC	ATCCATCGAAC	ccrdAarc 259
δ	147 rThrValProAl	coAlaAsnLysGlyT	TyrAlaSerSerAl	alleGlnThrLeuPheThrGl 166
Op	260 TACTGAACC	CAGTGAATAAAGGTT	Areacearreracade	TACTGAACCAGTGAATAAAGGTTATGGCGGTTCTACAGCCATCCAAAGCTTTTTCAAA 317
č	166 yProValLysAl	/sAlaGluGluProThrProThrP	hrProThrProLysIl	
Ωp	318 -GAATCTA	AAAGCTGAAGAA	AccccaAdGT	ceccaagetacttaagaagaggaaggaa 367
ò	186 SLYSLYSAS	anAlaAspProGl	uGluIleAsnSerSerAl	aProArgAspAspAspProGl 206
QQ	368 GAAGAAGA	ATCCTAATCCCGAGG	AAGTAAACTCTTCAAC	GAAGAAGAATCCTAATCCCGAGGAAGTAAACTCTTCAACTCCGGGTGGAGATGACTCAGA 427
à	206 uAsnArgSe	erLysPheTyrGluS	erAlaSerAlaArgLy	sArgThrValThrAlaGluGl 226
qq	428 GAACCGCT	caaagriciacgaga	Grectrorectadaa	cecricaaagriiciaceaeagaecriiciecracaaagaeaacreraacrecaeagga 487
ò	226 uArgGluA	rgAlaIleAsnAlaA	uarggluargalaileasnalaalaalysThrPheGluProThrAsnProPhePh	OThrasnProPhePheArgVa 246
qq	488 AAGAGAGAG	<u>aagagagagccgrcaargcagccaaaacattcgaa</u>	ccaaaacattcgaacc	ccaacaarccrracrrragagr 547
ò	246 lValLeuA	euArgProSerTyrLeuT	euTyrArgGlyCysIleMet	tTyrLeuProSerGlyPheAl 266
ą	548 TGTTCTGC	SACCATCATATCTAT	acadaddrigcarcar	IGTICIGCGACCAICAIAICIAIACAGAGGIIGCAICAIGIACIIGCCAICIGGGIIIGC 607
ò	266 aGluLysTy	BTyrLeuSerGly11eS	erGlyPhelleLysValGl	GlnLeuAlaGluLysGlnTr 286
qq	608 TGAGAATI	ACCTAAGTGGGATAT	creerricarcaaecr	gagaaatacctaagtgggatatctggtftcatcagcrccagcrcggrgagaaatg 667
λõ	286 pProValArg	rgCysLeuTyrLysAl	laGlyArgAlaLysPheSerGlnGl	TrpTyrGluPh 30
οqα	668 GCCAGTGA	serecerciacaad	ccagtgaggtgcctctacaaagcaggaggctaagtttagccaagga	TAGCCAAGGATGGTATGAGTT 727

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701 bp mRNA linear EST 10-JUL-2003
Brassica napus cDNA clone BN25045C06, mRNA
                                                                                                                                                                                     358
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Brassica napus (rape)

Brassica napus

Brassica napus

Brassica napus

Brassica napus

Brassica Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases I to 701)
                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                          359 GATGAATGCATCTCCCAGCACTTCAGAATTTGTTTGGTGGGTCTAAACTTAACAACTGC 418
                                                                                                                                                                                                                                                                                                                                                                           160
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Tel: 33 1 69 47 54 10
Exar: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
         AlaPheSerValTyrIlePheAanLeuSerHisSerGluIleAsnTyrHisSerThrGly
                                                                                                                                                                  242 GCTTTCAGTGTTAGTATTTAATTTGTACAACTCGGAAATAAACTATCAGACTAATGCC
                                                                                                                                                                                                                                              GluAspAla------GluValIlePheProSerSerValTyrProSerPro
                                                                                                                                                                                                                                                                                                                                                                           144 Leu------ProGluSerThrValProAlaAsnLysGlyTyrAlaSerSerAlaile
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                                                                                                                             LeuMetAspSerAlaHisAsnHisPheLysArgAlaArgLeuPheGluAspLeuGluAsp
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Genoplante
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Eb Gossypium raimondii cDNA clone GR_Eb0039N17
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                                                                                                                                                                                                                                                                                                                                                           Gossypium raimondii
Gossypium raimondii
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyte
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
I (baess 1 to 906)
Kim, H., Yu, Y., Kudrna, D., Haffield, J., Stum, D., Mueller, C.,
Udall, J. A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
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189
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54
23
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721
Tel: 520 625 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate: 0039 row: N column: 17.
Location/Qualifiers
1. 906
/organism="Gossypium raimondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/molumondi:"/mol
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3', mRNA sequence.
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CO108220.1 GI:48806906
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Query Match:
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Contact: Genoscope
Genoscope - Centre National de Sequencage
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BP 191 91006 EVRY cedex - France
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGY INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
                                                                                       Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; endicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Craud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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/clone_lib="Arabidopsis thaliana Adult vegetative tissue
Col-0"
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http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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835 ACAGCCATCCAAAGCTTTTTCAAA---GAATCTAAAGCTGAAGAA-----ACGCCC
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/ecotype="Col-0"
/db xref="taxon:3702"
/clone="GSLTLS48ZH11"
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Location/Qualifiers
                                                           1. .701.
/organism="Brassica napus"
/mol type="mRNA"
/cultivar="det Neuf"
/db_xref="taxon:3708"
/clone="MS2045C06"
/tissue_type="seed"
/clone_lib="BN25"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 IGCTTTCAGTGTTAGTATTTAATTTGTACAACTCGGAAATAAACTATCAGACTAATGC 301
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                                                                                                                                                                                                                                                                                                                       28 rLysPheLysAapGluLeuSerValAlaValAlaCeuThrValProAspGlyHisValTr
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TTCATCTGCTGGACGTGAAGATGATGTTGATATGCGCTTTAGATGTTATGAAAGTGCTTC
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| TCGAGTCAAATTGCATACTTCAGGTTCAGGTGCAATGAAACCAGAA.-------
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Mismatches:
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58.68%
45.16%
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Best Local Similarity:
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| Moj_type="MRNA" |
| Moj_type="MRNA" |
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| / Clone="GR Eb0039N11" |
| / Clone="Type="floral" |
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3', mRNA sequence.
                                                                237
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Gossypium raimondii
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Viridiplantae, Streptophyta; Eubryophyta; Tracheophyta;
Trosida; eurosida II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases I to 834)
Kim, H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Vidall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
                                                                                                                                                                                           548
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                                                                                                                                                                                                                                                                                                                     LysValGlnLeuAlaGluLysGlnTrpProValArgCysLeuTyrLysAlaGlyArgAla 297
                                                                                                                                                                                                                                 ArgiysArgThrValThrAlaGluGluArgGluArgAlaIleAsnAlaAlaLysThrPhe
                                                                                      LysPheSerGlnGlyTrpTyrGluPheThrLeuGluAsnAsnLeuGlyGluGlyAspVal
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Global assembly of Cotton ESTs
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Bullaing Room 303, Tucson, AZ, 85721-0036, USA
Fat: 520 626 9595
Fax: 520 621 1259
Fax: 520 621 1259
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    .834
    /organism="Gossypium raimondii"

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CD823066 645 bp mRNA linear EST 10-JUL-2003
BN25.047120F020109 BN25 Brassica napus cDNA clone BN25047120, mRNA
sequence.
                                                                                                                                                                                                                                                                                                                                                                             Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 645)
Genoplante.
Genoplante.
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                                                                                                                                                                                                                                                                                                                            144 uProGluSerThrValProAlaAsnLysGlyTyrAlaSerSerAla---IleGlnThrLe 163
                                                                        183
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Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                gglyarglyslyslysanalaaspProglugluIleAsnSerSerAlaProArgAspAs
                                                                                                                                                                                                                                                                                                      223 rAlaGluGluArgGluArgAlaIleAsnAlaAlaLysThrPheGluProThrAsnProPh
                                                                                                                                                                                                                              203 paspProGluasnArgSerLysPheTyrGluSerAlaSerAlaArgLysArgThrValTh
                         274 -CCTGAATCTACTGAACCAGTGAATAAAGGTTATGGCGGTTCTACAGACATCCAAAGGTT
                                                                          163 uPheThrGlyProValLysAlaGluGluProThrProThrProLysIleProLysLysAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 rGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysVal 279
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Mismatches:
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Arabidopsis thaliana (Unale Cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatrophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 669)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Diarg scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Diarg scale analysis of Arabidopsis full-length cDNA (2002b)
Fax: 81-298-36-9060
Britch Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4159
Fax: 81-298-36-4159
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     AV821829 RAFL4 Arabidopsis thaliana cDNA clone RAFL04-16-P22 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 AGCTCTTATGCAAATGGATTCCGCACAGAATCAGTTCAACAAACGTGCTCGATTGTTAA
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                                                                                                                   Arabidopsis thaliana (thale cress)
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AV821829.1 GI:19863860
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8 & f	GATGAC Thrala	Alignment Pred. No.: Score: Percent Si	Scores: milarity:	
7	CLGGAAGAGCCGIICAAAGIICIACGAGAGIGCIICIGCGAGAAAGAGAGAG	Best Lo Query M DB:	<pre>ty: 57.19* Mismatches:</pre>	
අු	123 GAGGAAAGAGAGAGGCCATTAATGCAGCCAAAACGTTCGAGCCAACAAAACCTTTCTTC 182	US-10-0	-088-187A-11 (1-341) x CO094348 (1-834)	
& a	245 ArgValValLeuArgProSerTyrLeuTyrArgGlyCysIleMetTyrLeuProSerGly 264	දු පු	67 GluPheValAspArgTyrSerlleArg1leGlyTyrLeuLeullePheArgTyrGluGly 86	
Sp qq	265 PheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysValGlnLeuAlaGluLys 284	& 8	87 AsnSerAlaPheSerValTyrIlePheAsnLeuSerHisSerGluIleAsnTyrHisSer 1(	106
SP GS	285 GlnTrpProValArgCysLeuTyrLysAlaGlyArgAlaLysPheSerGlnGlyTrpTyr 304	<i>ኤ</i> 8	107 ThrGlyLeuMetAspSerAlaHisAsnHisPheLysArgAlaArgLeuPheGluAspLeu 12	9 6
φα	305 GlupheThrLeuGluAsnAsnLeuGlyGluGlyAspValCysValPheGluLeuLeuArg 324	<b>상</b> 염	127 GludspGludspAlaGluValIlePheProSerSerValTyrProSerProLeuProGlu 146        ::::: 180 GAAGACGATGAATGC194	46 94
çç qa	325 ThrArgaspPheValLeuLysValThrAlaPheArgValAsn 338	ò a	147 SerThrValProAlaAsnLysGlyTyrAlaSerSerAlaIleGlnThrLeuPheThrGly 166	66
RESULT 15		ò	166166	و
LOCUS DEFINITION		qa	28 TCCAAACTTAACCATTGCGTTAATTGGAGCGGTGAAGTTAACCTTAATGCAGCAAAAGC 2	87
ACCESSION VERSION	MRNA sequence. CO094348 CO094348.1 GI:48793034	강 옵	167ProValLysAlaGluGluProThrProThrProLysIle 179	oυ 44
SOURCE ORGANISM	Gossypium raimondii Gossypium raimondii Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tra	ος O	180 ProLysLysArgGlyArgLysLysAsnAlaAspProGluGluIleAsnSerSerAla 19	99
REFERENCE AUTHORS	Spermacopnyta; Magnollophyta; eudlcotyledons; core eudlcots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium. 1 (bases 1 to 834) Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,	දු පු	200 ProargaspaspasperogluasnargserLysPheTyrGluseralaaseralaargLys 219 11	o 4
TITLE	Odali, J. A., Kapp, K.A., Wendel, J.F., Rao, K., Soderlund, C. and Wing, R.A. Global assembly of Cotton ESTs Unpublished (2004)	ò a	220 ArgThrValThrAlaGluGluArgGluArgAlaIleAsnAlaAlaLysThrPheGluPro 239	o 4
COMMENT	Contact: Kod A. Wing Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ, 85721-0036, USA	oy B	240 ThrasnProPhePheArgValValLeuArgProSerTyrLeuTyrArgGlyCysIleMet 259 :::	où 44
e de de de de de de de de de de de de de	Tel: 520 626 9595 Tel: 520 621 1259 Email: http://genome.arizona.edu Plate: 16 row: G column: 14.	o d	260 TyrLeuProSerGlyPheAlaGluLysTyrLeuSerGlyIleSerGlyPheIleLysVal 279	<u>о</u> н
ŭ	Location,Qualifiers  i. 834 /organism="Gossypium raimondii" /mol_type="mRNA"	දු පු	280 GlnLeuAlaGluLysGlnTrpProValArgCysLeuTyrLysAlaGlyArgAlaLy8 298	<b>®</b> ∺
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	w	λō	319 ValPheGluLeuLeuArgThrArgAepPheValLeuLysValThrAlaPheArgVal 337	
	ECORV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into NotI-EV. Colonies	<b>Q</b>	762 GTCTTCGAGCTGCTTAGATCGAGGGANGTCGTGCTTAAAGTGACTGTATTCCGTGTA 818	

Search completed: December 30, 2004, 09:49:31 Job time : 6758 secs

us-10-088-187a-11.rst

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AY661659 Sorghum b
AC097280 Oryza sat
AL954829 Oryza sat
AF104919 Arabidops
AC07504 Arabidops
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AJ47012 Medicago
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AC18491 Rattus no
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AC113213 Rattue no
AR415176 Sequence
AX972010 Sequence
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Makaryota, Varidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                              Arabidops
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Methods and means for modification of
characteristics
Patent: WO 0121822-A 10 29-MAR-2001;
Plant Bioscience Limited (GB)
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100.0%; Pred. No. 2.3
:ive 0; Mismatches
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Sequence 10 from Patent W00121822.
AX101036
AX101036.1 GI:13619892
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AR415176
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Compugen Ltd.
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/product="reduced vernalization response 1"
/protein id="AAM76973.1"
/db_xref="GI:21734796"
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KRTVTAEBERERAINAAKTFEPTNFFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGF
IKVOLAEKÇMPVRCLYKAGRAKFSQGWYEFTLENNLGBEDVCVFELLRTRDFVLKVTA
FRVNEYV"
   Arzegusz 1538 bp mRNA linear PLN 05-NOV-2003
Arabidopsis thaliana reduced vernalization response 1 (VRN1) mRNA,
VRN.-Ler allele, complete cds:
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                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheo
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
rosids, eurosids III, Brassicales, Brassicaceae, Arabidopsie.
1 (bases 1 to 1538)
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note="contains two VP1/ABI3-like B3 domains"
                                                                                                                                                                                                                                                                                    2 (bases 1 to 1538)
Levy, Y.Y., Gendall, A.R. and Dean, C.
VRN1, a gene required for response to vernalization
Unpublished
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                                                                                                                                                                                                           Levy, Y.Y., Mesnage, S., Mylne, J.S., Multiple roles of Arabidopsis VRN1
                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (23-JUL-2000) Molecular
Colney Lane, Norwich, Norfolk NR4
Location/Qualifiers
                                                                                                            Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/mol_type="mRNA"
/db_xref="taxon:3702"
/ch_omosome="3"
                                                                              GI:21734795
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/allele="Ler"
312. .1337
/gene="VRN1"
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Levy, Y.Y. and Dean, C.
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Best Local Similarity 100.
Matches 1027; Conservative
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                                                                                AGGGTCCCAGATAAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTTGCTGTTGCACTC
                                                                                                               ACAGTACCTGATGGTCATGTTTGGCGTGTAGGACTAAGGAAAGCTGACAAAATTTGG
                                                                                                                                             TTTCAAGATGGTTGGCAAGAGTTTGTTGACCGTTACTCCATTCGCATTGGTTATCTTTTG
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                                                                                                                                                                                                                                            <u> ATTTTTAGATATGAAGGAAACTCTGCCTTCAGCGTCTACATTTTCAATTTATCCCACTCT</u>
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TTTCAAGATGGTTGGCAAGAGTTTGTTGACCGTTACTCCATTCGCATTGGTTATCTTTTG

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AUTHORS Inze,D., de Veylder,L. and Vlieghe,K.  TITLE Identification of novel e2f target genes and use thereof JOURNAL Patent: WO 2004035798-A 1817 29-APR-2004;  CropDesign N.V. (BE)  FEATURES Location/Qualifiers 1.1026 /organism="Arabidopsis thaliana" /mol_type="unassigned DNA"  ORIGIN  ORIGIN	Query Match 99.9%; Score 1026; DB 6; Length 1026; Best Local Similarity 100.0%; Pred. No. 4.38-287; Matches 1026; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 ATGCCACGCCTTTCTTCCATAAGTTGATTTTCTCATCCACTATCCAAGAAAAACGTCTG 60	Qy         61 AGGGTCCCAGATAAGTTTGTGAGTAAATTCAAGGATGGGTTTTCGGTTGCTGTTGCACTC         120           Db         61 AGGGTCCCAGATAAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTTGCTGTTGCACTC         120	Qy         121 ACAGTACCTGATGGTCATGTTTGGCGTGTAGGACTAAGGAAAGCTGACAACAAAATTTGG 180           Db         121 ACAGTACCTGATGGTCATGTTTGGCGTGTAGGAACTAAGGAAAGCTGACAAAAATTTGG 180	Qy         181 TITCAAGAIGGITGGCAAGAGTITGITGACCGITACTCCATTGGATTGG	Qy 241 ATTTTAGATATGAAGGAAACTCTGCCTTCAGCGTCTACATTTTCAATTTATCCCACTCT 300	Qy 301 GAGATCAATTACCATTCCACGGTCTCATGGATTCGGCTCACACACGTTCAAACGGCC 360	Oy 361 CGTTTGAAGACCTTGAAGATGAAGATGCCGAGGTCATCCTTCCT	Qy         421         CCATCACCACTTCCTGAGTCTACAGTACCAGCCAACAAGGGTATGCTAGTTCAGCCATC         480           L	OY 481 CARACCTTGTTCACTGGACCAGTTARAGCTGAAGAGCCAACGCCAACCCCAAAAATACCT 540 Db 481 CARACCTTGTTCACTGGACCAGTTARAGCTGAAGAGCCAACGCCAACCCCAAAAATACCT 540	QY         541 AAAAGAGAGGAGGAGGAAGAAAAAAGTGCTGATCCTGAGGAAATAAACTCATCAGCTCCG 600           DD         541 AAAAAGAGAGGAGGAGAAGAAAAAATGCTGATCCTGAGGAAATAAACTCATCAGCTCCG 600	Qy 601 CGAGATGATCCAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAG 660	0   0   0   0   0   0   0   0   0   0
	dy         361 CGTTTGTTGAAGACCTTGAAGATGAAGATGCCGAGGTCATCTTCCTTC	OY 421 CCATCACCACTTCCTGAGTCTACAGTACCAACAACAGGTATGCTAGTTCAGCCATC 480	Qy     481 CAAACCTTGTTCACTGGACCAGTTAAAGCTGAAGAGCCAACGCCAAAAATACCT 540       D     192 CAAACCTTGTTCACTGGACCAGTTAAAGCTGAAGAGCCAACGCCAACCCCAAAATACCT 851	OY 541 AAAAGAGAGGAGGAAGAAAAAATGCTGATCCTGAGGAAATAACTCATCAGCTCCG 600	Qy       601 CGAGATGATGATCAGAGAACCGTTCAAAGTTCTACGAGAGAGGGGGGGG	OY 661 ACCGTGACTGCAGAAGAAGAGAGCGATCAATGCAGCCAAAAGGTTCGAACCAACA 720	Oy 721 AACCCTTTCTTCAGAGTTCTGCGACCATCCTATCTATACAGAGGTTGCATCATGTAT 780	OY 781 CTTCCTTCTGGGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAGTCCGG 840	Qy     841     CTTGCCGAGAAACAATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGT     900       Db     1152     CTTGCCGAAAAACAATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGT     1211	OY 901 CAAGANGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGAGACGCTGTGTTT 960	Qy         961 GAGCTGCTCAGAAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTAC 1020           Db         1272 GAGCTGCTCAGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTAC 1331	Oy 1021 GTCTGAA 1027                 Db 1332 GTCTGAA 1338	RESULT 3 CQ805406 LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS DEPINITION Sequence 1817 from Patent W02004035798. DEPINITION Sequence 1817 from Patent W02004035798. DEPINITION Sequence 1817 from Patent W02004035798.  CQ805406.1 GI:47111337 TABIOOPSIS thaliana (thale cress) SOURCE Arabidopsis thaliana CRGANISM Arabidopsis thaliana CRGANISM Arabidopsis thaliana Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="vrn1-2 mutation"
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                                              CAAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTTTT
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Plant Bioscience Limited (GB)
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/note="vrn1-1 mutation"
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ilarity 99.9%; Pred. No. 6.7e-287;
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Db 421 ACCGC 425  QY 469 AGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAAGCTGAAGAGCCAACG 522  Db 426TTCAGCCATCCAGAGCTTCTTCACTGGACCTGTTAAACCTGAAGAGGAACACCAACA 483	CTGAG CTGAG CTGAG CTGAG	QY         640 AGTGCTTCTGCGAGAAAGAGAACCGTGACTGCAGAAGAAGAGAGAG		Oy 760 TACAGAGGTTGCATCATGTATCTTCTGGGTTTGCTGAGAAGTACCTAAGTGGGATC 819	QY 820 TCCGGGTTCATCAAAGTCCAGCTTGCGGAGAAACAATGGCCTGTTCGATGTCTCTACAAA 879	Qy         880         GCCGGGGAGAGCCAAATTCAGTCAAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGA         939           Db         844         GCAGGGAGAGCTAAGTTCAGTCAAGGTTAGATATCACTGTGAGAATAACCTAGGA         903	Qy 940 GAAGGAGACGTCTGTGTGTTTGAGCTGCTCAGAACCAGAGATTTCGTTTTGAAAGTGACA 999			LOCUS  MY517929  BERSHITTON Brassica rapa cultivar Kwonsim reduced vernalization response 1  ACCESSION AY517929	_	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Tosida; eurosida II; Brassicales; Brassicaceae; Brassica. (равея 1 го 940)	AUTHORS Kwon, SJ., Park, BS., Kim, SY., Choi, HS., Lee, MC., Kim, JS., Lee, SI., Lim, KB., Kim, JA., Lee, MR., Jin, YM., Kim, D. and Kim, HI. TITLE Brassica rana Kwonsin Urwa mana	SE RS	. 0	Republic of Korea FEATURES Location/Qualifiers Source 1990 /organism="Brassica rapa"

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760 TACAGAGGTTGCATCATGTATCTTCCTGGGTTTGCTGAGAAGTACCTAAGTGGGATC 819	0 0	904 GAAGGICATCIGCGIGITIGAGCIGCTGAGAACCAGAGATTICGTTTTGAAAGTGACG 963 1000 GCCTTTCGAGTCAACGAGTACGTCTGA 1026 1010 GCCTTTCGAGTCAACGAGTACGTCTGA 1026 964 GCCTATCGAGTCAACGAGTACGTCTGA 990	RESULT 8 AF289051 LOCUS AF289051 5000 bp DNA linear PLN 05-NOV-2003 DEFINITION Arabidopsis thaliana reduced vernalization response 1 (VRN1) gene,		Eukaryota, Vilidiplantae, Sitreptophyta; Embryophyta; Tracheophyta; Eparatophyta; Magnoliophyta; editoctyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaces, Arabidopsis.  1 (bases I to 5000) AUTHORS Levy, Y. Y., Mesnage, S., Mylne, J.S., Gendall, A.R. and Dean, C.  TILLE Multiple roles of Arabidopsis VRNI in vernalization and flowering		S F S	TITLE Direct Submission JOURNAL Submitted (23-JUL-2000) Molecular Genetics, John Innes Centre, Colney Lane, Norvich, Norfolk NR4 7UH, UK	rce	/directionsoome="3" /chromosome="3" /map="between mi339 and m560B2" /ecotype="Landsberg erecta" <1879>4370		/gane="YKAN"" /gllele="Ler" /gln(18791938,31203567,36643732,38324031, 41224370) /gene="YRN1" /gene="YRN1" /note="Contains two VD1/AR13-like R3 Acmains"	/noton_start=1 /codon_start=1 /product="reduced vernalization response 1" /protein_id="AAM76972.1"

Location/Qualifiers  179186 /organism="Arabidopsis thaliana" /mol_type="cenomic DNA" /mb_xref="taxon:3702" /chromosome="3" /clone="K13E13" /clone="K13E13" /clone="Columbia" /sectype="Columbia" /sectype="Columbia" /seme id:K13E13.1 /note="unnamed protein product; gb AAC69119.1	/codon_start=1 /evidence=not_experimental /protein_id="alab01681." /b_xref="GI:9280309" /db_xref="GI:9280309" /tasslation="wkT1080LPNDLVBEILCRVPATSLRRIRSTCKAWNRLFKGDRI /Lasslation="wkT1080LPNDLVBEILCRVPATSLRRIRSTCKAWNRLFKGDRI LASKHFREKAKORRSLRNUYRRIPPISFNLHGNSPSLELKSELIDPHSKNSAAPFEI SRVIHCKGLLLCSSQLDESRVVWNPLTGETRWIRTGDFRQKGRSFDVGYYQKDKRS WTESRYLLCYRGTKKTEITYDPSDSORWILDDIJARGSIGSSELSVUKRSTKGNTYWFAK GYTERRPRTISLLKEPFYTEKSVPVLLPYGSRRLFQASSLSVVREDKLSVLLQLDGSS KTBIWVTNVIDETTKGAVSWTKVLALDLSPHLQIGNDGSFFLGEDKKVVMFCEKLIDE NKYKDMYIVGEDNVYTEVGFGUDEWDGCRAVILNYVPSLVQIERAGGNRKRGH" complement (2742 3977)	/note="unmaned protein product; gb AAF01602.1 gane id:Kl1813.2 similar to unknown protein" /codon_start=1 /evidence=not experimental /protein id="BAB01689.1" /protein id="BAB01689.1" /protein id="BAB01689.1" /protein id="BAB01689.1" /protein id="BAB01689.1" /protein id="BAB01689.1" /protein id="BAB01689.1" /protein id="BAB01168FIERPERRERRECRERELHIGSAGATESSDLRS REPERBOVYVILAAPLISREFIEGIDEWIRSHINCTRATHIGSAGATESBOLRS REPRESSERVITELCIDEWIRSHINGAPTINDOGIRASVUEDSREPPIM ARIRPSLDDERNAILIRGEITESRSNWATAADTINDOGIRASVUEDSREPPIM ARIRPSLDDERNAILIRGEITESRSNWATAADTINDOGIRASVUEDSREPPIM ARIRPSLDDERNAILIRGEITESRSNWATASTWARGSPFGNLISKRE LIKRSYSFECERESSERVTWEPATVSPWRYRRSTWARGSPFGNLISKREPPIM ARIRPSLDDERNAILIRGEITESRSNWATASTWARGSPFGNLISKREPPIM ARIRPSLDDERNAILIRGEITESRSNWATASTWARGSPFGNLISKREPPIM ARIRPSLSAMOVFPPISERIPATGSSSRRTKSMTSPWFRATAPHSSSRLRCGDP BALLSPREWRRRDTCAEW* Complement (join(57135792,58836006,61126349,6779667966796679. Anote="unmamed protein product; gene_id:Kl3E13.3 unknown protein id="BAB01690.1" /dorte="unmamed protein product; gene_id:Kl3E13.3 /note="unmamed protein product; gene_id:Kl3E13.3 /note="unmamed protein languages of the langu	RVWKDLKDHTGFKSTSGLVKAIVITGDNRIFTGHQDGKIRVWRGSKRRTGGYSRIGSL PTLAEFLIKSVANPRAYVBFNRRKNVLKTHYDAVGSCISLINEEGLIKSGSMDKTLKVW RLSDSKCLESIQAHDDAINTVAAGPDDLLFTGSADGTLKWWRELGGKGTKHFLVWVL MKQBNAVTALAVNITAAVVYCGSSDGTVNFWEGQKYLSHGGTLRGHRLAVLCLAAAGS IVLLSGGADKVICWRRNDGSHSCLSVLWDHVGFVKCLTAVEDDGEGHREKGDQKWIV YSGSLDKSVKVWWVTESASTVIG"  1926319350  /product="Codon recognized: UAC; gene_id:K13E13.5"
FEATURES source CDS	S G	S S S S S S S S S S S S S S S S S S S	t KNA
QY         763 AGAGGTTGCATCAT         776           Db         4017 AGAGGTTGCATCATGGTAATAAAAAACATCTTAGGAAGACTTAATCTTATCGGTGTCTT         4076           QY         777	Qy         953 CAATGGCCTGTTCGATGTCTTCTACAAACCGGGAGAGCCAATTCAGTCAAGGATGGTAC         912           Db         4197 CAATGGCTGTTCGATGTCTTCACAAAGCCGGAGAGCCAATTCAGTTCAGTTCAGTTGTTCAGTTCAGTTGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTTCAGAACAACTTAGGAGAACATTTCAGAACAACTTAGAAAGAA	APOUOT35 /c APOUOT35 ARDIGOPS THAILAND TO THE THE THE THE THE THE THE THE THE THE	Denmark, http://www.cbs.dtu.dk/services/Netcene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremlinl.zool.isatate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between-neighboring submissions. The 5' clone is MCB22 and the 3' clone is MHP21.

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                                          /trānslation="MGBLDEAPIQAPEHRPNTHLTNSGDFIFSDEIPTIDLSSLEDTH
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                                                                                                                                                        VCQEYAREVEKLAPRLIBLVSISLGLPGDRLTGFFNEQTSFLRFNHYPPCPNPELALG
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SAEHRVVVNTSKERPSIPFPPPSHEANIEPLEELISEENPPCYKKYNWGKFFVSRNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCACAGTACCTGATGGTCATGTTTGGCGTGTAGGGAAAGGAAAGGAAAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                          .1e-178;
                                                                                                                                                                                                                                                                                                                                                                               Score 653.4; DB Pred. No. 2.1e-17 0; Mismatches
           xref="GI:9280317"
                                                                                                                                                                                                                                                                                                                                                                               Query Match 63.6%;
Best Local Similarity 77.2%;
Matches 969; Conservative
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                                                                                                                                                                                                                                                  /note="unnamed protein product; gb|AAC72857.1 gene id:k13813.7 gene id:k13813.7 /codon starf=1
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/ protein id= "BAB01694.1"
/ drotein id= "BAB01694
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/db_xref="G1:9280316"
/translation="MNSAHWHFRARLFEDLEDEDAEVIFPSSVYPSFLPESTVPANK
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SASARKRYTVABERERAINAAKTPEPTNPFRYVLRPSYLYRGCIMYLPSGPAEKYLS
GISGFIKVQLAEKQWPVRCLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFV
LKVTARRVNEYV"
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TDTTWVCVLSAISQTGLLEIGSLVHGYIEKLGFTPEVDVFIGTALVDMYSKCGCLNNA
FSVFELMKVKRVFTWTSMATGLALNGRONETPNLLNRVAESGIKPNEITFFSLLSAYR
HIGLVEBGIELFKSKTRFGYTPVIEHYGCIVDLLGKAGRIGBAYQFILAMFIKPDAI
LLRSLCNACSIYGETVMGEBIGKALLEIEREDEKLISGSECEDYVALSNVLAHKGKWVB
VEKLRKEMKERRIKTRPGYSFV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MVTTQNTKARVTSVSHRRSQQDPESPVKKFFKLVLPSTMKDKAM
FIPRFFWKLQGSKLSRVVTLBTPAGFKRSIKLKRIGESIWFHEGWSERARAHSIEEGH
FILFEYRENGSFRVII TRVVSACETKYPLDAVHIIDSDDDIIDITGKEFDTEHKSKKRS
RDIELDKIILHDLDVWNPWHVLKEEBEDKRVFRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MSSVFPGPRFLSLLQQNSKTLIQAKQIHAQLVINGCHDNSLFGK/
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LLYLMERTFVFVLGACARSASSSALRVGRIVHGMYKKLGFLYESELIGTTLLHFYAKN
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[Ante="unmand protein product; gb|AAD43153.1 gene id: Atl3B13.10 similar to unknown protein"
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gene_id:K13E13.9
similar to unknown protein"
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/note="unnamed protein product; gb|AAF15933.1
foote="unnamed protein product; gb|AAF15933.1
eimilar to unknown protein"
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/evidence=not_experimental
19930. .20860
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                                                                                                                     id:K13E13.6
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/evidence=not_e
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                                                                              /note="gb
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3357 TCTGAGATCAATTACCATTCCACCGGTCTCATGGATTCCGCTCACAACCACTTCAAACGC 3416 358 GCCGTTTGTTTGAAGACCTTGAAGATGAAGATGCCGAGGTCATCTTTCTT		QY         793 TITGCTGAGAGTACCTAAGTGGGATCTCCGGGTTCATCAAGTCCGGGAGAAA 852           Db         4137 TITGCTGAGAGTACCTAAGTGGGATCTCCGGGTTCATCAGGGAGAAA 4196           QY         853 CAATGGCCTGTCTCACAAAGCCGGGAGAGCCAAATTCAGTCAAGGATGCTAC         912           Db         4197 CAATGGCCTGTTCTACAAAGCCGGAGAGCCAAATTCAGTCAAGGATGCTAC         4256           QY         913 GAATTCACTCTACAAGACAACTTAGGAAAGCCGGAAGCCAAATTCAGTCAAGGATGCTCAAGGATGCTCAAGGATGCTCAAGGATGCTCAAGAATTCAGTCAAGGATGCTCAAGAATTCAGTCAAGGATGCTCAAGAATTCAGTCAAGAAATTCAGTTTAGAACACTTAAGAAGAAGAAGAAGAACAACTTAAGAAGAAGAAGAACAACTTAAGAAGAAGAACAACTTAAGAAGAAGAACAACTTAAGAAGAAGAACAACTTAAGAAGAAGAACAACTTAAGAAAAACTTAAAAAAAA
8 6 8 6 8 6 8 6 8 6 8 6 8	8 4 8 4 8 4 8 4 8 4 8 4 8 8 8 8 8 8 8 8	OY  OY  OY  OY  OY  OY  OY  OY  AY042868  LOCUS  DEFINITION  ACCESSION
Qy         763 AGAGGTTGCATCAT	AX101027 LOCUS AX101027 LOCUS AX101027	Owery Match         63.6%; Score 653; DB 6; Length 5000;           Best Local Similarity         77.1%; Pred. No. 1.9e-178;           Matches 968; Conservative 1; Mismatches 1; Indels 285; Gaps 3;           Qy         58 CTGAGGGTCCAGATAAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTGTGTGT

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16234 TICATCTITCATTATTATATATATATAGAGCACTTCTGAGGTGAATTATCAGTCTGC 16293
Direct Submission
Submitted (12-DEC-2002) Shusei Sato, Kazusa DNA Research Institute,
Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu,
Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp,
URL.http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243777 bp DNA linear HTG 13-AUG-2004 truncatula clone mth2-23j1, WORKING DRAFT SEQUENCE, 17
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
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Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (03-DEC-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16114 TTGGCGTGTAGGGTTAAAGAAGGCCGACAACAGAATTTGGTTTGCTGATGGTTGGGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16174 ATTIGITICAACGCTACACCATIGGCATIGGATACTTTTTAGTATTCAIGTATAGAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15994 TACGAATATTTTGAAGCCAACTTGTATTTTTGAATTGCAGGGGATTCCGGACAATTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16054 GAGGAAATATGGCGGTCAGCTTTCAACAATTGCTACCCTCACTGTTCCAGATGGTACTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGTAAATTCAAGGATGAGCTTTCGGTTGCTGTTGCACTCACAGTACCTGATGGTCATGT
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Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-23j1
                                                                                                                                   1. .78589
/organism="Lotus corniculatus var. japonicus"
/organism="Lotus corniculatus var. japonicus"
/oll type="genomic DNA"
/variety="japonicus"
/db_xref="taxon:34305"
/chromosome="2"
/clone="lign3H18"
/clone="lib="lign"
/clone="lib="lign"
/olone:"TAC clone:TM0262-synonym: Lotus japonicus"
                                                                                                                                                                                                                                                                                                                                                    Length 78589;
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                                                                                                                                                                                                                                                                                                                                                  13.7%; Score 140.4; DB 8;
llarity 66.6%; Pred. No. 4.4e-29;
Conservative 0; Mismatches 101;
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AC137825 22 G1:50897368
HIG; HTGS_PHASE1; HTGS_DRAFT.
Medicago truncatula (barrel medic)
Medicago truncatula
                                                                                                                  Location/Qualifiers
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                                                                                                                  28676 TCCCGGTAAGTATCAGAGACAGACTCTTAATTACGTATTAACTTTTGTTTCAGAGGAGAG 28735
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                                                                                                                                                                                                                                                                                                                                                                                        TCTTCAGAGTGGTTCTGCGACCATCCTATACAGAGGTTGCATCAT-------
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Lotus corniculatus var. japonicus
Bukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophy
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicuts;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 CTACATITICAATITATCCCACTCTGAGATCAATTACCATTCCACGGTCTCATGGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 CGAGGTCATCTTTCCTTCTTGTGTACCCATCACCACTTCCTGAGTCTACAGTACCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 CAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Length 125021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Join(28449. .28680,28766. .28965,29065. .29313)
/gene="IIJR21.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 201; Indels 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8e-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="Hypothetical Protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 270.4;
Pred. No. 6.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /proteIn_id="AAD43152.1"
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                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Unknown Protein"
                                                                                                                                                                                                                                                                                                                                                                                        /gene="F13F21.7"
23803. .26346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F13F21.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                         23803. .26346
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26.3%;
Best Local Similarity 62.1%;
Matches 694; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28523 TAAGGĪCATTĀĀTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28449.
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                                                                                                                                                                                                                                                                                                                                                                gene
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   join(6527. .6667,6772. .6859,7159. .7311,7597. .7757,
7840. .8514,8612. .8939,9020. .9240,9369. .9546,9658. .10142)
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/mote="Hypothetical Protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NXICOLSPOLEKFLGTSQLARTEVVKKWMAYIREHDLQDFTNRRNILCDESLHSLFRV
KTINMFQONKALAKHIWALNDGDGCFKNYKEBDVDBTSGERDEKDVKIEBALENNEEE
SREEDBESVRKRKRKRKRKRESEKPKKGGGFTKVCSLSPELQAFTGTPQLARTEV
KMLWKYIKENNLQDPSDEKTILCDESLRSLFPVESINMFQWNKQLAKHIWPLVQEDEA
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Complement (15762. 16883)
/gene="F13F21.5"
/gene="F13F21.5"
/gene="F13F21.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="WAMSHLFLSSSPQSSLALRLHSTTQFTLSYSKNNKDCSPQSANE
AKVSKRSLLCRAIHMESGHSGEQPKKLNFDNLLRRTKHVWDNSPQPVKEFPWNRAFGN
FIQLVLDLAISVVKFLFVPILAVSSISEMSYCAHERKLALVPFPLVIGMVVAGVLQET
ALKISPRLKEAEVPWHLIAMMFFTLIKLPGPYYPYWGRLLVPHFANGVLIRALWSMF
                                                                                                                                                                                                                                                                             /trānslation="MSENTKVEAKRVPIGAGCNRVNNNVSWGASGLVSFGAQNAVAVF
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NNDVKFPYSRSDLSFPAVSLLSLIPKECKVVCLDSICVUTKAIVTLSLAELPQNPGRF
ALALGGLDNKIKLYSGERTGKTSVCELKGHTDWIRSLDFSLPLHTTEEIPNSIMLVS
SSQDKVIRIWKLVYGDVGSWRREITLARYIEGPPFYGGTFTYQISVEGYLIGHEDW
YSVEWQPPVIDFIDGRLVNHQPLSILSASMDKTWMIWRPEKKTGVWVNVCVGELSHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALGPYGGHWSPNSLSTLAHGYGGAFHLWRNYSSKESENWOMOKVPSGHPAAVTDVTW
ARTGEYLLSVSQDQTTRVFSAWKNDEGNEAEDEHWHELARPQVHGHDINCVAMVQGKG
NHRPVSGAEEKVVRVFEAPLSFLKTLMHTCAGGEGSFPEDLQADVQVLGANMSALGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHGNELFSLCSDHKGNLVASSCKAQSASMAEIWLWEVGTWKAVGRLQSHSLTVTHLEF
SYDDTLLLSVSRDRHFSVFSIQRTDNGEVSHKLMAKVEAHKRIIWACSWNPFGHQFAT
SSRDKTVKIWSVENDARIKQILVLPPFGSSVTAVAWTGLDRNEKSGCVAVGMESGLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAACAVEMIHAASLILDDLPCMDDDSLRRGKPTWHKVPGEKTISILASNALRSLAVKQT
LASTSLGVTSSERVLRAVQEMRAVAVTEGLVACQAADLAGERBYSFKUEDDELBYLLELMH
VHKTAVLVEAAAVVQAAIMGGGSDEETERLKSYARCVGLMFQVMDDVLDETKSSEELGK
TAGKDLITGKLIYPKVMGVDNAREYAKRLNREAQEHLQGFDSDKVVPLLSLADYIVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSNVKI I ETEEGTTATAALALRLEPFMCHVSAVNRLAWRPTEKCESNQSLRWLTSCGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tränslation="MRPRYSLILSAMRLIRPSNRRLSSIASSDSEFISYMKNKAKSIN
KALDNSIPLCNNFVPLWEPVLEVHKAMRYTLLPGGKRVRPMLCLVACELVGGQESTAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tränslation="MVSDSDLVTQLREILRSSDLETTTPASVRRQLEVYFGVELTDKK
AFVREQIDAFLESDALLESKPEQEEEDCNGDQNDEEGSENDDDKTELPVKAKKRGGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QKPIYLHSSSEPLERNGGGEGLDTFETVPEAAPAELKEPPIEDQLAFHTLWPESHKLY
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12784. .12898,12987. .13143,13236. .13410,13500. .13602,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="F13F21.3"
complement(10370. .11380)
/gene="F13F21.3"
/note="F13F21.3"
/note="F3 identical to geranyl geranyl pyrophosphate
synthase [Arabidopsis thaliana] gi|2578822."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product=="gerany1 gerany1 pyrophosphate synthase"
/protein_id="AAD43148.1"
/db_xref="GI:6430748"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="F13F21.4"
/note="Hypothetical Protein"
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/db_xref="GI:5430747"
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21730. .21921
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Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                       507
                                                                                                                                                                                                                                                                                                                               567
                                                                                                                                                                                                                                                                                                                                                                                                                   627
                                                                                                                                                                                                                                                                                                                                                                                                                                              399 CCTAATCCCGAGGAAGTAAACTCTTCAACTCCCGGTGGAGATGACTCAGAGAACCGCTCA 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    638
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                                                                                                                                                                                         246 GATGCTAAGGTCATTTATC-------CATCGATCCTGAATCTACTGAA 287
                                                                                                                                                                                                                                                                                   CCAGTGAATAAAGGTTATGGCGGTTCTACAGACATCCAAAGCTTTTTCAAAGAATCTAAA 347
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                130 ATCCTCCACACTCTGAGATCAACCACC---ATTCTAGTAGTGAAGCTCTTATGCAAATG 185
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                                                                                                                                                                                                                                                                                                                               GCTGAAGAGCCAACGCCAACCCCAAAATACCTAAAAAGAGAGGGGAGGAAGAAGAAAAT
                                                                                                                                                                                                                                                                                                                                                         519 GCCGTCAATGCAGCCAAAACATTCGAACCAACAAATCCTTACTTTAGAGTTGTTCTGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTAAGTGGGATCTCCGGGTTCATCAAAGTCCAGCTTGCGGAGAAACAATGGCCTGTTCGA
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                                                                                                        186 GATTCCGCACAGAATCAGTTCAACAAACGTGCTCGATTGTTTGAAGATCCTGAACTCAAA
                                                                                                                                                 GATGCCGAGGTCATCTTCCTTCTGTGTACCCATCACCACTTCCTGAGTCTACAGTA
                                                                                                                                                                                                                                       CCAGCCAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                     568 GCTGATCCTGAGGAAATAAACTCATCAGCTCCGCGAGATGATGATCCAGÁGAACCGTTCA
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Stress-regulated genes of plants, transgenic plants containing same, and methods of use
Patent: WO 0216655-A 273 28-FBB-2002;
The Scripps Research Institute (US); Syngenta Participations A (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    579 ccarcararcraracadaderrecarcareracraecarcrederrrecreadaarac
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    681
    organism="Arabidopsis thaliana"

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Sequence 273 from Patent WO0216655.
AX505578.1 GI:23386815
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                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; roside; euroside II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1146)

S Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M., Ralin-Neumann,G., Southwick,A., Lam,B., Miranda,M., Chenk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.

L Submitted (25-JUN-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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//productions
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PIKLQUGEKQMPVRCLYKAGRAKFSQGWYEFTLENNIGEGDVCVFELLRTRDFVLEVT
APRVNEYV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 CGTTACTCCATTCGCATTGGTTATCTTTTTAGATATGAAGGAAACTCTGCCTTC 270.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen,M., Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shinn,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 GGACTAAGGAAAGCCAACAAAATCTGGTTTCAAGACGGTTGGCAGGAGTTTGTCAAC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN arbidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIs. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                       e-mail for correspondence: arab@sequence.stanford.edu
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Pred. No. 2.8e-117;
0; Mismatches 194;
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/organism="Arabidopsis thaliana"
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/db Xref="taxon:3702"
/chromosome="!"
/clone="RAPL04-16-P22"
      FLI_CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/gene="F13F21.8"
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/codon_start=1
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J. VLARED L. L. C. LEDNAY, A.B., CONN, L., Hansen, N.F., Altafi, M. Araujo, R., Fuizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Submission Bubmitted (08-JUN-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pederspiel, N.A., Fall, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, B., Dunn, P., Gonzalez, A., Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotekkala, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
Submitted (09-UL-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                         Chases 1 to 125021)

Pederspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
                                                                                                                                                                                                                                                                                                              Submitted (06-MAY-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304
Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriuni, M., Vysotskaia, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTACCAGCCAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTT
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                                                                                                                                           Length 681;
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                                                                                                                                        Score 397.6; DB 6;
Pred. No. 3.2e-104;
0; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                         67 AAAGATGCTAAGGTCATTAATCCATCGAAC----
                                DNA"
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/db_xref="taxon:3702"
                                                                                                                                           Query Match
Best Local Similarity 76.6%;
Matches 538; Conservative
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on Jul 9, 1999 this sequence version replaced gi:5019265.

e-mail for correspondence: arabésequence.stanford.edu

Genes with similarity to proteins in the databases are described

as 'putentive'. 'like' or 'similar to'. Genes that have EST

similarity but no significant protein similarity are described as

'unknown proteins'. Genes that are annotated based only on gene

prediction software are described as 'hypothetical proteins'.

The software programs used to predict genes include: Grail

(Informatics Group, Oak Ridge National Laboratory,

http://compbio.ornl.gov/section/index.html), GENSCAN (Chris Burge,

http://gromic.stanford.edu.chris/GENSCANW html), Fexa (V.Solovyev

& A.Salamov, Sanger Centre, http://genomic.sanger.ac.uk/),

NetPlantGene (S. M. Hebsgaard, et al., CBS, Technical University of

Denmark, http://www.cbs.dtu.dk/NetPlantGene.html) and

eWotif(Nevill-Manning, C.G. Wu, T.D. & Brutlag, D.L.,

http://motif.stanford.edu/projects.html);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein id="AAD43146.1"
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PLN 30-0CT-2002

AC007504 125021 bp DNA / linear PLN 30-OCT Arabidopsis thaliana chromosome I BAC F13F21 genomic sequence,

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 12502)
Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P.,

REFERENCE AUTHORS

Arabidopsis thaliana (thale cress) Arabidopsis thaliana

AC007504.3 GI:5430745

ACCESSION VERSION KEYWORDS SOURCE, ORGANISM

complete sequence.

AC007504 LOCUS DEFINITION

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RESULT 13

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155466 TGGTGGTGATATTTCTCCAACTGTTACTCTCACAGTTCCTGATGGCAGTGTGTGGCGTGT 155407
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3 (bases 1 to 243777)
Shaull, S., Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B.,
Cook, D., Xim, D. and Roe, B.A.
Direct Submission
Submitted (13-AUG-2004) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 CAAGGATGAGCTTTCGGTTGCTGTTGCACTCACAGTACCTGATGGTCATGTTTGGCGTGT 149
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                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                    OK 73019, USA
On Aug 3, 2004 this sequence version replaced gi:50540779
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150 AGGACTAAGGAAAGCTGACAACAAAATTTGGTTTCAAGATGGTTGGCAAGAGTTTGTTGA
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Rice gene Tumour su Gene enco

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Aav74539 Staphyloc Ach21644 Human adu Aax40160 Gastric c

Human gen Human pol

Aba06788 F Abv84125 F Abs06776 G Abs06778 F Abv84123 F Abv84123 F Acf72703 S Aca2033 F Aca2033 F Aca2045 F Aca20464 F

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Novel VRN1 polynucleotide sequence encoding a polypeptide which alters vernalization response of plant in which VRN1 nucleic acid is expressed. useful for influencing and assessing vernalization phenotype of plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of Arabidopsis thaliana VRNI. This protein is capable of altering the vernalisation responses of a plant. Also provided are a number of PCR primers used to isolate the sequences. The sequences are useful in the
                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                         VRN1; vernalisation; flowering; crop; ss.
                                   ADM03188
ABA98590
ADB80383
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ADC03457
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ABA06788
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/*tag= a
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                         AAK51957
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                                                                                                                                                                                                                                                                                                                                       A thaliana VRN1 coding sequence.
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Arabidopsis thaliana.
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P-PSDB; AAB35491.
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production of crop plants, where they are able to control the timing of flowering, the duration of vernalisation required, the optimum temperature, or even eliminate the need for vernalisation completely. The present sequence is the VRNI coding sequence
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                                                                                                                       AGGGTCCCAGATAAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTTGCTGTTGCACTC
                                                                                                                                                              ACAGTACCTGATGGTCATGTTTGGCGTGTAGGACTAAGGAAAAGCTGACAAAATTTTGG
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                                                                                                                                                                                                                                                                                                                    0
                                                                      Length 1495;
                                                 G; 458 T; 0 U; 0 Other;
                                                                                          Indels
                                                                     ; Score 1027; DB 4;
; Pred. No. 6.1e-312;
0; Mismatches 0;
                                                    Seguence 1495 BP; 403 A; 322 C; 312
                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1027; Conservative 0;
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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up or down-regulated in transgenic plants overexpressing the heterodimeric or down-regulated in transgenic plants overexpressing the heterodimeric cor down factoristics accordingly. The present invention describes alter plant characteristics accordingly. The present invention describes corpy, therepouts and animal feed products, where generating transgenic plants for the production of growth regulators. CC charymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal or physiology, altered endoreduplication, biochemistry, signal or passive to the corresponding wild type plants. Accordingly, these cach relative to the corresponding wild type plants. Accordingly, these contrains also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell cole in a variety of biological processes such as DNA replication, cell cole in a variety of biological processes such as DNA replication, cell colescentification as transcription factors. This polymucleotide sequence is thate cress cDNA repressed 1.3 fold or more in plants overexpressing the EZFA/DPa
                                                            1169 CAAGGAIGGIACGAAITCACICIAGAGAACAACITAGGAGAAGGAGACGICIGIGIGII 1228
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                                       GAGCTGCTCAGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAACCAACGAGTAC
                                                                                                                                                                                                                                                                                                                                                                            Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 1817.
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                                                                                                                                                                                                                                                                                                                                                                                                                  gene; 88; plant; transgenic; B2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabol:
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100.0%; Pred. No. 1e-311;
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P-PSDB; ADN73923.
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Best Local Similarity
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Mismatches

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Matches 1026; Conservative

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                  Arabidopsis thaliana DNA fragment SEQ ID NO: 25332
                                 AAC39629 standard; DNA; 1510 BP
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9905-0130891P-
9905-0132048P-
9905-0132484P-
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9905-0132487P-
9905-0134256P-
9905-0134219P-
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23-APR-1999;
28-APR-1999;
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04-MAY-1999;
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18-MAY-1999;
19-MAY-1999;
21-MAY-1999;
24-MAY-1999;
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09-MAR-1999;
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16-APR-1999;
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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944 AACCGTGACTGCAGAAGAAGAAGAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCAAC 1003
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                CCATCACCACTTCCTGAGTCTACAGTACCAGCCAACAAAGGGTATGCTAGTTCAGCCAT
                                                                                           CCAAACCTTGTTCACTGGACCAGTTAAAGCTGAAGAGCCAACGCCAACCCCAAAATACC
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3597 ATCTATCGCTGATTACGCGTCTTATCATTCTTTTGAGGTTGATGCTTGATATTTTCCTTA 3656
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               Sequence 5000 BP; 1447 A; 871 C; 931 G; 1750 T; 0 U; 1 Other;
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1; Mismatches 1;
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                                          Query Match 63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of Arabidopsis thaliana VRN1. This protein is capable of altering the vernalisation responses of a plant. Also provided are a number of PCR primers used to isolate the sequences. The sequences are useful in the production of crop plants, where they are able to control the timing of Ilowering, the duration of vernalisation required, the optimum temperature, or even eliminate the need for vernalisation completely. The present sequence is the VRN1 gene
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                                           CGCGAGATGATGATCCAGAGAACCGTTCAAAGTTCTACGAGAGAGTGCTTCTGCGAGAAAG
                                                                                             AGTCAAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTG
                                                                                                                                  TATCTTCCTTCTGGGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAGTC
                                                                                                                                                                                                                 TATCTTCCTTCTGGGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTC
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CCTAAAAAGAGGAGGAAGAAGAAAAATGCTGATCCTGAGGAAATAAACTCATCAGCT
                                                                               AGAACCGTGACTGCAGAAGAAGAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCA
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                         CCGCGAGATGATCCAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAG
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   4077 CACTGAICTCTAAAAGAAGCCTICTGTTTCTGTTTCTCTCAACAGTAICTTCCTTCTGGG 4136
                            Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                    TTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAGTCCAGCTTGCGGAGAAA
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                                  Query Match 53.4%; Score 548.4; DB 3; Best Local Similarity 99.8%; Pred. No. 1.7e-161; Matches 549; Conservative 0; Mismatches 1;
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08-0CT-1999

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05-MAR-1999;
09-MAR-1999;
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                                                                                                                              GGACTAAGGAAAGCCAACAAAATCTGGTTTCAAGACGGTTGGCAGGAGTTTGTCAAC
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                                                                                                                                                CGTTACTCCATTCCATTGCTTATCTTTTGATTTTTAGATATGAAGGAAACTCTGCCTTC
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99US-016132DP.
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73.5%;
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Best Local Similarity
Matches 646; Conserv
26-OCT-1999;
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss. Arabidopsis thaliana DNA fragment SEQ ID NO: 18041.

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23 - 70N - 1999;

24 - 70N - 1999;

27 - 70N - 1999;
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	re 439.4; DB 3; Length 1344; d. No. 4.7e-127; Migmatches 196; Indels 38; Gaps 5;	GGACTAAGGAAAGCTGACAAAATTTGGTTTCAAGATGGTTGGCAAGAGTTTGTTGAC 210 	CCATTCGCATTGGTTATCTTTTGATTTTTAGATGAAGGAAACTCTGCCTTC 270
9905-0149929P. 9905-0149902P. 9905-0149902P. 9905-0150864P. 9905-0151066P. 9905-0151066P. 9905-0151066P. 9905-0151066P. 9905-0151080P. 9905-015130P. 9905-0151319P. 9905-0151319P. 9905-015403P. 9905-015403P. 9905-015403P. 9905-015403P. 9905-015403P. 9905-015403P. 9905-01553P. 9905-01553P. 9905-01553P. 9905-01553P. 9905-01553P. 9905-01553P. 9905-015933P. 9905-015933P. 9905-015933P. 9905-015933P. 9905-015933P. 9905-015933P. 9905-015933P. 9905-015933P. 9905-01694P. 9905-01694P. 9905-016094P. 9905-016094P. 9905-016094P. 9905-016094P. 9905-016094P. 9905-016094P. 9905-016094P. 9905-016094P. 9905-016094P. 9905-016094P. 9905-016094P. 9905-016094P.	42.8%; Sco arity 73.4%; Pre onservative 0;	ggactaaggaaagctgacaacaa; 	GTTACTCCATTCGCATTGGTTA'                        GTTTCTCCATTCGGATTGGT
20-AUG-1999; 23-AUG-1999; 25-AUG-1999; 26-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 28-EEP-1999; 28-EEP-1999; 28-EEP-1999; 29-EEP-1999; 29-EEP-1999; 21-CCT-1999; 21-CCT-1999; 21-CCT-1999; 21-CCT-1999; 21-CCT-1999; 22-CCT-1999; 23-CCT-1999; 23-CCT-1999; 24-CCT-1999; 25-CCT-1999; 25-CCT-1999; 26-CCT-1999; 27-CCT-1999; 28-CCT-1999; 28-CCT-1999; 28-CCT-1999; 28-CCT-1999;	Query Match Best Local Simil Matches 645; C	151 GGA      226 GGA	211 CGT      286 CGT
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271 AGCGTCTACATTTTCAATTTATCCCACTCTGAGATCAATTACCATTCCACGGTCTCATG 330

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342 ATCCTCCACACTCTGAGATCAACCACC----ATTCTAGTGAGGTGAAGCTCTTATGCAAATG 397

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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynuclectides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynuclectides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                 Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAACCGTGACTGCAGAAGAAAAAGAGAG 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGCCGTCAATGCAGCCAAAACATTCGAACCAACAAATCCTTACTTTAGAGTTGTTCTG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGIGCCICTACAAAGCAGGGAGAGAGTTAAGCCAAGGAIGGIATGAGTICACACTC 579
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                                                                                                                                                                                                                                                                                                                                                                                    Score 397.6; DB 6; Length 681;
Pred. No. 4.6e-114;
0; Mismatches 134; Indels 30;
                                                                                                                                             Claim 144; SEQ ID NO 273; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                           Sequence 681 BP; 217 A; 139 C; 162 G; 163 T; 0 U; 0 Other;
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    (SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA PARTICIPATIONS
                                             Wang X,
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Best Local Similarity 76.6%;
Matches 538; Conservative
                                             Kreps J,
                                                                        WPI; 2002-304127/34
                                            Harper JF,
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                   GATGCCGAGGTCATCTTCCTTCTTCTGTACCCATCACCACTTCCTGAGTCTACAGTA
                                                                                                             CCAGCCAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAA
                                                                                                                                                                     GCTGAAGAGCCCAACGCCCAAAAATACCTAAAAAGAGAGGAGGAAGAAGAAAAT
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22-JUN-2001; 2001US-0300111P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention describes an Arabidopsis thaliana nucleic acid (I). The polypeptide (II) encoded by (I), transgenic plant (III) or genetically modified cell (IV) are useful for screening a candidate agent for its biological effect, by combining the acadidate agent with (II), (III) or (IV), and determining the effect of the candidate agent on (II), (III) or (IV). (I) is useful for identifying homologous or related genes, for producing compositions that modulate the expression or function of its encoded protein, for mapping functional regions of the protein, in diagnosis, for studying associated physiological pathways, for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic organisms, such as plant cells and plants.
                                                                                                                                                                Transgenic plant; plant; genetically modified cell; environmental stress; ribozyme creation; disease resistance; stress tolerance; fungicide screening; insecticide screening; gene; ds.
 580 GAGAACAATATAGGCGAAGGAGATGTATGTGTTTTGAGCTACTCAGAACTCGGGATTTC 639
                                                                                                                                              Arabidopsis thaliana expressed sequence related polynucleotide #237,
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JP, Haas V
Hoffman N;
                    GTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTACGTCTGA 1026
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Ledford BL, Woessner
, Davis KR, Allen K,
                              640 GTTCTCGAAGTCACCGCCTTTCGTGTCAATGAGTATGTGTGA 681
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A, Mathew AV, I
er M, Slater T,
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ABX62122 standard; DNA; 426 BP.
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                                                                                                                           25-FEB-2003 (first entry)
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Page A, Ma
Kricker M,
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GARCIA C A.
KRICKER M.
SLATER T.
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MATHEW A V.
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ALLEN K.
HOFFMAN N.
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                                                                                                                                                                                                       Unidentified.
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Garcia CA,
Hurban P;
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manipulation of cells, preferably plant cells, in screening assays of various plant strains to determine the strains that are capable of withstanding a particular disease or environmental stress, for enhancing or inhibiting production of biosynthetic product in a plant, for producing polypeptides, as probes for the detection of mRNA in biological samples, to generate ribozymes or oligonuclectides, and to create genetically modified and forming oligonuclectides, and to create genetically modified and cransgenic organisms, such as plant cells and plants. (II) or (III) is transgenic organisms, such as plant cells and plants. (II) or (III) is cusful for introducing or improving disease resistance and stress tolerance in plants, screening biological active agents, e.g., fungicides, insecticides, etc., and for elucidating biochemical pathways. (III) is useful as crops for their enhanced diseased resistance, enhanced traits of interest, for screening programs, as crops which exhibit captance represents a nucleic acid that may correspond to naturally sequence represents a nucleic acid that may correspond to naturally cocurring Arabidopsis thaliana expressed sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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99US-0130449P.
99US-0130510P.
99US-0130891P.
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04-MAY-1999;
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 The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid arepresentative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to ablotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                     1843 AAGGAAAGCCAACAACAAATCTGGTTTCAAGACGGTTGGCAGGAGTTTGTCAACCGTTT 1902
                                                                                                                                                                                                                                                                                                                                                                 1784 reaccrirca diriniris cacita cantaccida recidante residentia de de 1842
                                                                 Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
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                                                                                                                                                                                                                                                                                                                                                                                        156 AAGGAAAGCTGACAAAAATTTGGTTTCAAGATGGTTGGCAAGAGTTTGTTGACCGTTA 215
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                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                  Claim 144; SEQ ID NO 2973; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                              Score 101; DB 6; Length 2000;
Pred. No. 1.8e-20;
                                                                                                                                                                                                                                                                         Sequence 2000 BP; 619 A; 273 C; 344 G; 764 T; 0 U; 0 Other;
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                      Zhu T;
(SYGN ) SYNGENTA PARTICIPATIONS AG.
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                      Harper JF, Kreps J, Wang X,
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99US-0123180P.
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                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.3
Matches 121, Conservative
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                                          WPI; 2002-304127/34
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01-APR-1999;
06-APR-1999;
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23-MAR-1999;
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05-MAR-1999,
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19-JUL-1999;
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23-JUL-1999;
23-JUL-1999;
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23-JUL-1999;
                                                                                                                 26-JUL-1999;
27-JUL-1999;
27-JUL-1999;
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28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                              TITGIGAGIAAATICAAGGATGAGCTITCGGTTGCTGTTGCACTCACAGIACCTGATGGT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                        232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195
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                                                                                                                                                                                                                                                                                                                                                                                                     113 TTCTTCAAGTTGGTCTTACCTTCAACGATGAAGATAAGATGATGAGAGATTCCGCCAAGG 172
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Pred. No. 8.5e-10;
0; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX62454 standard; DNA; 411 BP
          990S-01593299
990S-0159330P
990S-0159631P
990S-0159638P
990S-0160741P
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Best Local Similarity 51.3
Matches 154; Conservative
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13-0CT-1999;

14-0CT-1999;

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21-0CT-1999;

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22-0CT-1999;

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22-0CT-1999;

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26-0CT-1999;

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26-0CT-1999;

26-0CT-1999;

26-0CT-1999;

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28-0CT-1999;

28-0CT-1999;
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HAMILTON C M.
                                         WOESSNER J P
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                            RAMEAKA J G.
                                  MATHEW A V.
LEDFORD B L.
                   PRICE J L.
RAINES T M.
         GORLACH J.
                                                     SLATER T.
DAVIS K R.
ALLEN K.
                                                               HOFFMAN N.
HURBAN P.
                                                                        An Y,
                                                  KRICKER M.
                                            HAAS W D.
                               PAGE A.
                                                                        Gorlach J,
                                                           (ALLE/)
(HOFF/)
                                                                  (HURB/)
         GORL/)
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(DAVI/)
                            (RAME/)
                      RAIN/)
                HAMI/
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                               PAGE/
                                      LEDF/
                                            HAAS/
                                                  KRIC/
                                               GARC/
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Claim 1; SEQ ID NO 569; 43pp; English.
Rameaka JG, Page A, Mathew AV,
Garcia CA, Kricker M, Slater T,
Hurban P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic organisms, such as plant cells and plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             withstanding a particular disease or environmental stress, for enhancing or inhibiting production of biosynthetic product in a plant, for producing polypeptides, as probes for the detection of mRNA in biological samples, to generate additional copies of (I), to generate ribozymes or oligonucleotides, as single stranded DNA probes or as triple-strand transgenic originals, such as plant cells and plants. (II) is useful for introducing or improving disease resistance and stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tolerance in plants, screening biological active agents, e.g., fungicides, insecticides, etc., and for elucidating biochemical pathways. (III) is useful as crops for their enhanced diseased resistance, enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           traits of interest, for screening programs, as crops which exhibit enhanced tolerance to environmental stress, or to produce a factor. This sequence represents a nucleic acid that may correspond to naturally occurring Arabidopsis thaliana expressed sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at sequence.uspto.gov/sequence.html?DocID=999909770423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Price JL, Raines TM, Yu Y;
Ledford BL, Woessner JP, Haas WD;
, Davis KR, Allen K, Hoffman N;
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27-JAN-2000; 2000US-0178512P.
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411 GAAGGAGATGTATATGTGTTTGAGCTACTCGGGATTTCGTTCTCGAAGTCACC 352
                                                                                                                351 GCCTTTCGTGTCAATGAGTATGTGTGA 325
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                                                                              1000 GCCTTTCGAGTCAACGAGTACGTCTGA
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FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463 Patent No. 5670367
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGY: linear
IMMEDIATE SOURCE:
                    2617
3294
3284
4200
4200
4200
90050
90050
485
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1141
2922
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US-08-232-463-14
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US-08-232-463-14/c
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Sequence 1, Appli
Sequence 1, Appli
Sequence 2145, Ap
Sequence 29582, A
Sequence 13580, A
Sequence 9, Appli
Sequence 9, Appli
Sequence 977, Appli
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Sequence 168, App
Sequence 1090, Ap
Sequence 15640, App
Sequence 549, App
Sequence 151, App
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Sequence 228, App
Sequence 228, App
Sequence 85, Appl
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Sequence 22, Appl
Sequence 14, Appl
                                                                                                  December 30, 2004, 12:43:00; Search time 113 Seconds (without alignments) 6460.002 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(/ggn2 6/ptodata1/lina/5A_COMB.seq:*

(/ggn2 6/ptodata1/lina/5B_COMB.seq:*

(/ggn2 6/ptodata1/lina/6A_COMB.seq:*

(/ggn2 6/ptodata1/lina/6B_COMB.seq:*

(/ggn2 6/ptodata1/lina/RB_COMB.seq:*

(/ggn2 6/ptodata1/lina/PCTUS COMB.seq:*

(/ggn2 6/ptodata1/lina/backfiles1.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-270-767-29582
US-09-270-767-13580
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US-08-961-527-168
US-09-221-017B-1090
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US-09-270-767-15640
US-09-799-451-549
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US-09-107-532A-1348
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US-08-956-171E-228
US-08-781-986A-228
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US-09-621-976-2813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-916-421B-1
US-09-692-570-1
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1027
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Maximum Match 100%
Listing first 45 summaries
                                                                    nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                                                                   Perfect score:
                                                                    OM nucleic
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                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                        Run on:
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No.
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Sequence 22,
Sequence 74,
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Sequence
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COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STREET: VA
US-08-430-024-1

US-08-702-1

US-09-017-302-1

US-08-923-992A-5

US-08-923-992A-5

US-08-923-992A-1

US-08-923-992A-1

US-08-923-992A-1

US-08-923-992A-1

US-08-923-992A-1

US-08-923-041-5

US-09-41-5

US-09-41-812A-4

US-09-411-812A-4

US-09-590-113-4

US-09-590-113-4

US-09-683-26B-74

US-09-683-26B-74

US-09-36B-708B-22

US-09-80-708B-22

US-09-80-708B-22

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |::: ::::||:| : ::: | : ::: 363 IYYWIWWITWWWYMWKKARM 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 CCAGCCAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 RWWSTYWYMAWGKKWWRYATTWRRAMMWWAAWTWMWYMWWWMCMSSRGAAMYRRTWMMW 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 AAAGAGAGGAAGAAGAAGAAAAAATGCTGATCCTGAGGAAATAAACTCATCAGCTCCGCG 602
                                                                                                                                                                        603 AGATGATGATCCAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAAAC 662
                                                                                                                                                                                                                                663 CGTGACTGCAGAAGAAGAGAGAGAGCCATCAATGCAGCCAAAAACGTTCGAACCAACAAA 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 MSTRWYCYMCWKCCMYRGRRCAWYTMARGRMWSYAWGKWKSMRSAMSMCTRMYYKKGSTY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 GAIGCCGAGGICAICTIICCIITCTICIGIGIACCCAICACCACTICCIGAGICIACAGIA 447
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                           Gaps
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                           Indels
                                                                                                                                                                                                                                                                                                                                                         FACENT NO. 08390

GENERAL INCORMATION:

APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JOHER, S. S.
APPLICANT: Giordano, J.Y.
ITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
Pred. No. 0.0066;
                           6; Conservative 148; Mismatches
                                                                                                                                                                                                                                                                                                                                  Sequence 2813, Application US/09621976
Patent No. 6639063
             2.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
                                                                                                                                                                                                                                                                                                        RESULT 2
US-09-621-976-2813/c
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RESULT 3

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NAME/KEY: promoter
LOCATION: (1)..(1141)
CTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
US-09-806-708B-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 RKVRRWVRTRGRMRNYMVAWBTAHRRRYNNGWTBAMAYRRWTWNNNNNAKAMCKRAKYW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGATCCAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAAACGTG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               596 WSHTWBHBRAGAAHYMWBMMYBAKCHCMKAWYKAKKYAGAGGSNNNNNNNNNNNNNNNN 655
Sequence 22, Application US/09806708B

Facent No. 6784342

GENERAL INFORMATION:
FAPLICATY: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
CURRENT APPLICATION NUMBER: US/09/806,708B

CURRENT FILING DATE: 2001-04-03
FRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 547 AGAGGGAGGAAGAAAAAAATGCTGATCCTGAGGAAATAAACTCATCAGCTCCGCGAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  667 ACTGCAGAAGAAAGA----GAGAGAGCCATCAATGCAGCCAAAAACGTTCGAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 TYKKARHBARWDWVWHSAWKKWHANAAHYSRKKWTBYKRKTWVNNNNGTTWWKRMWAWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TICCTICIGGGITIGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCAICAAAGTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 GWNRABVNSTCTTWKSKTTKVRTSCWANNCRAGDANKDHKWWKWSAAMGVYWNNNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  722 ACCCTTTCTTCAGAGTGGTTCTGCGACCATCCTATCTATACAGAGGTTGCATCATGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 TIGITCACTGGACCAGTTAAAGCTGAAGAGCCAACGCCAACCCCCAAAAATACCTAAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.9%; Score 40.2; DB 4;
ilarity 10.7%; Pred. No. 0.02;
Conservative 207; Mismatches 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1141
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Gil H. Choi
Parrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Farmon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2342 ATGAGGTTATAGATATCTACACCTGCCTCACCTGCAACCATTTCATCTTCGTTTACACGA 2283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2282 ATAACGATACGAGAAGCATCTACATATTCAATTACACCGCCACGGTTTGCGATTACACAC 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 AAGAGTTTGTTGACCGTTACTCCATTCGCATTGGTTATCTTTTGATTTTAGATATGAAG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 GAAACTCTGCCTTCAGCGTCTACATTTTCAATTTATCCCACTCTGAGATCAATTACCATT 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
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                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.5%; Score 35.8; DB 4; Length 4143; Best Local Similarity 52.3%; Pred. No. 1.1; Matches 79; Conservative 0; Mismatches 72; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINCATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIPICATION: cunknown>
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997.
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2222 ACACCAGAGTCACGTGCAACGTTCGCTTCCA 2192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 CCACCGGTCTCATGGATTCCGCTCACAACCA 347
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                     CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 228, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4488 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                           p ORGANISM: Acinetobacter baumannii
US-09-328-352-4006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (301) 309-84
INFORMATION FOR SEQ ID NO: 228:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Maryland COUNTRY: USA
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           FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-08-956-171E-228
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Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 TTTGTTGACCGTTACTCCATTCGCATTGGTTATCTTTTGATTTTTAGATATGAAGGAAAC 261
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                                                                                                                                                                                                                                            ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Rolease #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDIDATE OF CANDI
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS: FOLGY & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTER: 51
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid_
STRANDEDNESS: single
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                                                                                                                                       CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-328-352-4006/c
                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                              334 cagadacadeadadadadagantracaarcadeecadadadadeecadadadaaaaaada 393
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 228, Application US/08781986A
Sequence 228, Application US/08781986A
Sequence 228, Application US/08781986A
Settle No. 6737248
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTON: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADRESS:
ADRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      554 GGAAGAAGAAAATGCTGATCCTGAGGAAATAAACTCATCAGCTCCGCGAGATGATGAT 612
                                                                                                                                                                                                       554 GGAAGAAGAAAATGCTGATCCTGAGGAAATAAACTCATCAGCTCCGCGAGATGATGAT 612
                                                                                                                                                                                                                                                                                                                                    494 CTGGACCAGTTAAAGCTGAAGAGCCAACGCCAACCCCAAAAATACCTAAAAAGAGAGGA
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                                                                                                        Query Match
3.5%; Score 35.8; DB 4; Length 4488;
Best Local Similarity 56.3%; Pred. No. 1.1;
Matches 67; Conservative 0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: PP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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SEQUENCE DESCRIPTION: SEQ ID NO: 228:
US-08-956-171E-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/OCKET NUMBER: PB248
TELECOMMUNICATION INFORMATION:
TELEFAN: (301) 309-8504
TELEFAN: (301) 309-8514
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TELEFAN: (301) 309-8514
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Best Local Similarity
Matches 67; Conserv
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RESULT

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1964 ATACCCTTCTCCTCCACAAAAAGGGCTGAGGGGGGGGAGTCAAGTGAAAGGGTGCAAGCGA 2023
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US-09-621-976-2813
i Sequence 2813, Application US/09621976
j Patent No. 6639063;
GENERAL INFORMATION:
APPLICANT: Under Milne Edwards, J.B.
APPLICANT: JODERT, S.
APPLICANT: GLONGANO, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT PILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2084 TATGTATTGTCTTGATGTACTTAATATTACCTGAGTTTGA 2123
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,164
FILING DATE: July 17, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6218521men D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5499 - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATCTTCCTTCTGGGTTTGCTGAGAAGTACCTAAGTGGGA 817
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Pred. No. 1.5;
0; Mismatches
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (212) 838-354 TELEFAX: (212) 838-358 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3441 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 51.2
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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LOCATION: (234514)...(234814)
OCHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (309398)...(309398)
OCHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (309418)...(309418)
OCHER INFORMATION: n equals a, t,
OTHER INFORMATION: n equals
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LOCATION: (312837). (312837)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (312593). (312993)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (319226). (319226)
OTHER INFORMATION: n equals a, t
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature_LOCATION: (148948) .. (148948) OTHER INFORMATION: n equals a, t. NAME/KEY: misc_feature_LOCATION: (163385) .. (163385) OTHER INFORMATION: n equals a, t.
                                    n equals a,
                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a,
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LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc. feature
LOCATION: (234220)...(334220)
OTHER INFORMATION: n equals a,
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a,
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IION: (559167)..(559167)
R INFORMATION: n equals a,
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IION: (559241)..(559241)
R INFORMATION: n equals a,
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
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LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a,
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CON: (622708)..(622708)
INFORMATION: n equals a,
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                                                                                                                            NAME/KEY: misc feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals
                               OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (98159)..(98159) OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature_
LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals
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LOCATION: (657203)..(657203)
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LOCATION: (6009
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Patent No. 6503729
GRERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
FILE REFERENCE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR PELING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                     331 GATTCCGCTCACAACCACTTCAAACGCCCCGTTTGTTTGAAGACCTTGAAGATGAAGAT 390
                                                                                                                                                                                                                                                                                                                                                                                 391 GCCGAGGTCATCTTTCTTTCTGTGTACCCATCACCACTTCCTGAGTCTACAGTACCA 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 SKTSYKSMMMCWIRSHKYCYIKARWIGYYCYRKGGMWGKRGRWYASKKYMWKRWWWCWAR 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              571 GATCCTGAGGAAATAAACTCATCAGCTCCGCGAGATGATGATCCAGAGAACCGTTCAAAG 630
                                                                                                                                                                                                                                                                                                                  18 KWKWSWSYWMYWKWYYMKTYWRWRRKKKKAWWKYWKTWTWWYWRYAMWGTYKKKAMCRTK 77
                                                                                                                                                                                                                                   1;
                                                                                                                                                                                   DB 4; Length 832;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                              Query Match 3.4%; Score 34.6; DB 4; Pest Local Similarity 9.6%; Pred. No. 0.99; Matches 30; Conservative 153; Mismatches 127;
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LOCATION: (28222). (28222)
OTHER INFORMATION: n equals a,
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TYPE: DNA
ORGANISM: Homo sapiens
                                                  ; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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LENGTH: 1664976
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US-08-916-421B-1/C
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                                     547953 Addridgadarrangcdgararaagaararaharrirgadgadadgararacaaraha
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                                                                                                  NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals
FEATURE:
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals
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3.4%; Score 34.6; DB 4; Length 1
Best Local Similarity 48.3%; Pred. No. 80;
Matches 97; Conservative 0; Mismatches 104; Indels
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LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (68242)..(68242)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc feature
LOCATION: (71362)..(713652)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
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LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a,
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LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a,
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a,
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a,
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (674435)..(674435)
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RESULT 11
US-09-692-570-1/c

i Sequence 1, Application US/09692570

i Sequence 1, Application US/09692570

i Patent No. 679466

i GENERAL INFORMATION:

i APPLICANT: Bult et al.

i TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ Patent No. 6797466

i TITLE OF INVENTION: jannaschii

i TITLE OF INVENTION: jannaschii

i FILE REFERENCE: PB275C1

CURRENT APPLICATION NUMBER: US/09/692,570

CURRENT PILING DATE: 1996-08-22

i PRIOR PILING DATE: 1996-08-22

i PRIOR PILING DATE: 1997-08-22

i NUMBER OF SEQ ID NOS: 20

i SOFTWARE: Patentin version 3.1

i ENGTH: 1664976
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                                       626 CAAAGTICTACGAGAGTGCTICTGCGAGAAAGAGAGAACCGTGACTGCAGAAGAAGAGAGA
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LOCATION: (84773)..(84773)
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LOCATION: (312837)..(312837)
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LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t,
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LOCATION: (234187)..(234187)
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LOCATION: (234220)..(234220)
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LOCATION: (559]67)..(559167)
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LOCATION: (103998)..(103998)
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t,
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LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a,
                                                                                LOCATION: (98343) .. (98343)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a,
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LOCATION: (600992)..(600992)
                                                        NAME/KEY: misc feature
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LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c,
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ION: (855539)..(855539)
INFORMATION: n equals a, t,
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LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t,
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LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t,
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t,
                                             FRATURE:
NAME/KEY: misc feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
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LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a,
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LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
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LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (682442)...(682442)
OTHER INFORMATION: n equals
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LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals
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US-09-270-767-13580

j Sequence 13580, Application US/09270767

j Patent No. 6703491

j GENERAL INFORMATION:
    APPLICANT: Homburger et al.
    TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
    TITLE OF INVENTION: Nucleic 7326-094
    CURRENT PELING DATE: 1999-03-17
    NUMBER OF SEQ ID NOS: 62517
    SOFTWARE: PatentIn Ver. 2.0
    SOFTWARE: PatentIn Ver. 2.0
    SEQ ID NO 13580
    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                        Sequence 29582, Application US/09270767
Sequence 29582, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT Homburger et al.
APPLICANT HOMBURGER et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT PALLIAN NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29582
LENGTH: 710
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                                 Length 1494;
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Pred. No. 1.2;
0; Mismatches 138;
                                                                             41;
                                   Score 34.4; DB 4;
Pred. No. 1.6;
                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Drosophila melanogaster
US-09-270-767-29582
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Best Local Similarity 45.9%;
Matches 117; Conservative (
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                                     Query Match
Best Local Similarity 59.0%;
Matches 59; Conservative
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US-09-270-767-29582
US-09-107-532A-2145
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                 547834
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                                                                                                                                                                                                                                                                            506 AAGCTGAAGAGCCAACGCCAACCCCAAAATACCTAAAAAGAGAGGAGGAAGAAGAAAA
                                                                  Gaps
                      Length 1664976;
                          Score 34.6; DB 4; Length 1
Pred. No. 80;
0; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
COMPAGE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRICATION NUMBER: 60/085,598
PRILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: J197
ATTONNEY/AGENT INFORMATION:
NAME: ATINICATION NUMBER: 60/051571
ATTONNEY/AGENT INFORMATION:
NAME: ATINICATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...1494
SEQUENCE DESCRIPTION: SEQ ID NO: 2145:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                            547773 AACTCATAAATAAAGCGTATA 547753
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; Sequence 2145, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
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TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                    686 GAGCCATCAATGCAGCCAAAA 706
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SEQUENCE CHARACTERISTICS:
LENGTH: 1494 base pairs
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MOLECTLE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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                              3.4%;
Similarity 48.3%;
97; Conservative (
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Matches 97;
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APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IGA FC Binding Forms of the Group B TITLE OF INVENTION: Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
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                                                                    Query Match 3.3%; Score 34.2; DB 4; Length 1421; Best Local Similarity 45.9%; Pred. No. 1.8; Matches 117; Conservative 0; Mismatches 138; Indels 0
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
FILING DATE: 05-SEP-1997
CLASSIFICATION: 536
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,707
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRENCE/DOCKET NUMBER: 1438.0140001/RWE
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LEMOTH: 13492 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08923992A
Patent No. 6280738
; ORGANISM: Drosophila melanogaster
US-09-270-767-13580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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NAME/KEY:
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1: /cgm2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgm2_6/ptodata/1/pubpna/PCT_MEW_PUB.seq:*
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14: /cgm2_6/ptodata/1/pubpna/USO9E_PUBCOMB.seq:*
14: /cgm2_6/ptodata/1/pubpna/USOP_PUBCOMB.seq:*
15: /cgm2_6/ptodata/1/pubpna/USOP_PUBCOMB.seq:*
16: /cgm2_6/ptodata/1/pubpna/USOP_PUBCOMB.seq:*
17: /cgm2_6/ptodata/1/pubpna/USOP_PUBCOMB.seq:*
18: /cgm2_6/ptodata/1/pubpna/USOP_PUBCOMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	7 US-10-767-795-1318 Sequence 1318, Ap	. •	1 US-09-938-842A-273 Sequence 273, App	٠,			-	6 US-10-424-599-97592 Sequence 97592, A			7 US-10-767-795-1320 Sequence 1320, Ap	
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US-09-938-842A-2973 Sequence 2973	1 US-09-938-842A-2973 Sequence 2973,	US-IO-/39-930-3/43 Sequence 3/43, US-10-424-599-23571 Secuence 23571	7 US-10-767-795-1319 Sequence 1319,	b US-10-424-599-89606 Sequence 89606, At US-09-770-423-569 Sequence 569, At	6 US-10-424-599-64367 Sequence 64367,	6 US-10-424-599-64127 Sequence 6 US-10-424-599-36556 Sequence	1 US-09-732-627A-1636 Sequence 1636,	7 US-10-437-963-101386 Sequence 101386 6 HS-10-424-509-00156 Sequence 00156	7 US-10-767-795-1315 Sequence	7 US-10-437-963-49771 Sequence 49771,	6 US-10-424-599-124535 Sequence	8 US-10-425-115-130216 Sequence 7 HS-10-021-323-11719 Semience	7 US-10-437-963-3179 Sequence 3179,	US-09-938-842A-2527 Sequence	I US-09-938-84ZA-Z5Z/ Sequence Z5Z/, 8 IIS-10-425-115-69193 Sequence 69193	7 US-10-437-963-60237 Sequence 60237	7 US-10-437-963-35940 Sequence 35940	7 US-10-437-963-89631 Sequence 89631	/ US-10-43/-963-35166 Sequence 35166 7 118-10-437-963-86418 Sequence 86418	7 US-10-437-963-74762 Sequence 74762	8 US-10-425-115-89684 Sequence 89684	8 US-10-739-930-4151 Seguence 4151,	8 US-10-425-115-89685 Sequence 89685	6 US-10-424-599-47912 Sequence 47912	6 US-10-221-714A-288 Sequence 288,	ALIGNMENTS	/10767795 Acid Molecules and Other Molecules Associated Wand Uses Thereof For Plant Improvement B US/10/767,795 11-30 In GOSHI-09MAY01-C1540_1 In Score 405.6; DB 17; Length 1471; Pred: No. 5.5e-118;	matches 329
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TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3 CURRENT PAPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR PILING DATE: 2000-08-24 PRIOR PILING DATE: 2000-08-24 PRIOR PILING DATE: 2000-08-24 PRIOR PILING DATE: 2000-08-24 PRIOR PILING DATE: 2001-01-6 PRIOR PILING DATE: 2001-01-6 PRIOR PILING DATE: 2001-01-16 PRIOR PILING DATE: 2001-01-16 PRIOR PILING DATE: 2001-01-16 PRIOR PILING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379
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Best Local &
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RESULT 3 US-09-938-842A-273

Sequence 273, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
APPLICANT: Harper, Jeff APPLICANT: Wang, Xun APPLICANT: Wang, Xun APPLICANT: Zhu, Tong

RESULT 2 US-09-938-842A-273

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426 cricagagregricrecearcerecrareraracagagerecarerarerererer 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTACGTCTGAA 1027
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Pred. No. 3.8e-83;
0; Mismatches 3; Indels 0
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APPLICANT: Garcia, Carlos A.
APPLICANT: Slader, Maja
APPLICANT: Slader, Ted
APPLICANT: Allen, Keith R.
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: Hoffman, Neith
APPLICANT: WARFER: 2008 (PARA-01/PRV)
CURRENT APPLICATION NUMBER: US/09/770,423
CURRENT APPLICATION NUMBER: 60/178,512
PRIOR PILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 426
                                                        681
                                                        640 Gircicgaagicaccccriricgrercaargagiargrerga
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                                                                                                                                                                                         Sequence 237, Application US/09770423 Publication No. US20020040490A1 GENERAL INFORMATION:
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| LOCATION: (1)...(426)
| OTHER INFORMATION: n = A,T,C or
US-09-770-423-237
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
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Best Local Similarity 99.0%;
Matches 296; Conservative
                                                                                                                                                                                                                                                                           APPLICANT: Gorlach, Jorn
APPLICANT: An, Yong-Qiang
PELICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                 Yu, Yang
Rameaka, Joshua G.
  985 GTTTTGAAAGTGACAGCC
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                                                                 APPLICANT: Marper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Thu Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: STRESS-REGULATED OF USE
FILER REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR PLILING DATE: 2001-08-24
PRIOR PLILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-6-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 273
LENGTH: 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 GAAGAIGCCGAGGICAICTTICCTTCTTGTGTACCCATCACCACTTCCTGAGICTACA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 GTACCAGCCAACAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTT 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 GAACCAGTGAATAAAGGTTATGGCGGTTCTACAGCCATCCAAAGCTTTTTCAAAGAATCT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGCTGAAGAGCCAACGCCAACCCCCAAAAATACCTAAAAAGAGAGGAGGAAGAAGAAA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 AAAGCTGAAGA-----AACGCCCAAGGTACTTAAGAAGAGAGGAAGGAAGAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 rcaaagrrcracgagagrgcrrcrgcragaaagagaacrgraacrgcagaggaaagaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.7%; Score 397.6; DB 11; Best Local Similarity 76.6%; Pred. No. 1.2e-115; Matches 538; Conservative 0; Mismatches 134;
Sequence 273, Application US/09938842A Publication No. US20040009476A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Arabidopsis thaliana US-09-938-842A-273
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Sequence 1317, Application US/10767795

Fublication No. US20040181830A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Vongwei

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21 (55534) B

CURRENT APPLICATION NUMBER: US/10/767,795

CURRENT FILING DATE: 2004-01-30

NUMBER OF SEQ ID NOS: 117596

SEQ ID NO 1317
                                                                                                                                                                     957 TTACCATCATGCTTTGCTGAGAAGTATCTAAGTGGGGGTTTCGGGATTTATTAAACTTCAG 1016
                                                                                                                                                                                                                                                                                                  CTTCCAGATGGGAGACAATGGCCCGTTCGATGTCGCTATAGAGGTGGCAAAGCCAAGTTT 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        959 TTGAGCTGCTCAGAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGT 1018
                                              AACCCTTTCTCGCAGAGTTGTCTTACGACCATCATATCTATACCGGGGATGTATTATGTAC
                                                                                                                                                                                                                                          CTTGCGGA----GAAACAATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTC
                                                                                                                      CTTCCTTCTGGGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               603 AGATGATGATCCAGAGACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: CLone ID: GOSHI-09MAY01-C1540_2
US-10-767-795-1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 255.2; DB 17;
Pred. No. 4.6e-70;
0; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                AGTCAGGGATGGTACGAGTTTACGTTGGAGAATAA 1111
                                                                                                                                                                                                                                                                                                                                                                 AGTCAAGGATGGTACGAATTCACTCTAGAGAACAA 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 24.8%;
Best Local Similarity 73.0%;
Matches 356; Conservative C
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         Sequence 1316, Application US/10767795
Publication No. US20040181830A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53534)B
CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT PLING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NOS: 117596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Э;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ATTTTTAGATATGAAGGAAACTCTGCCTTCAGCGTCTACATTTTCAATTTATCCCACTCT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCGTGACTGCAGAAGAAAGAGAGAGAGCCATCAATGCCAGAAAAGGTTCGAACAAAA 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C1540 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 287.8;
Pred. No. 1.9
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Best Local Similarity 61.3%;
Matches 573; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-767-795-1316
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3

Gaps

602 223 662 283 722 343

782 403 841 463

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Sequence 9015, Application US/10021323

Publication No. US20040123340A1

GENERAL INFORMATION:

APPLICANT: Deikman, Jill

APPLICANT: Fincher, Karen L.

APPLICANT: Ziegler, Todd E.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(52274)B

CURRENT PILING DATE: 2001-12-12

PRIOR APPLICATION NUMBER: US 60/255, 619

PRIOR PILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 17880

SEQ ID NO 9015
     APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1186 TGTCCAACGGTAGACAGTGGTCTGTTCGCTGCCTCTATAGGGGAGGTCGAGCCAAGTTAA 1245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602 GAGATGATGATCCAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 662 CCGTGACTGCAGAAGAAAGAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCAACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 22.0%; Score 226.2; DB 16; Length 1760; Best Local Similarity 72.6%; Pred. No. 1.1e-60; Matches 307; Conservative 0; Mismatches 113; Indels 3;
                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59139C.1
US-10-424-599-97592
                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Glycine max
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APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 118105
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Pred. No. 6.2e-61;
0; Mismatches 123; Indels
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                                                                                                                                                                                                                                             Sequence 118105, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 71.4%;
Matches 314; Conservative C
                                                                         1019 ACGTCTGA 1026
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US-10-424-599-118105
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                                          FEATURE:
NAME/KEY: unsure
LOCATION: (1) .. (644)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3828-022-Q1-K6-E11
US-10-021-323-9015
                                                                                                                                                       Score 174.8; DB 17;
Pred. No. 1.6e-44;
0; Mismatches 223;
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Best Local Similarity 57.1%;
Matches 420; Conservative
              TYPE: DNA ORGANISM: Gossypium hirsutum
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; Sequence 97591, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION: APPLICANT: La Rosa Thomas J

US-10-424-599-97591

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Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       549 AGGGAGGAAGAAAAATGCTGATCCTGAGGAAATAAACTCATCAGCTCCGCGAGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 gchgcchchartgcccrarhgcritriarchahdrccarcricchagahacchaccrohd
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                                                    Other Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Zhou, Yihua TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Assitified Prince Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53534)B CURRENT APPLICATION NUMBER: US/10/767,795 CURRENT FILING DATE: 2004-01-30 NUMBER OF SEQ ID NOS: 117596 SEQ ID NO 1320
                                                       Acid Molecules and Other Molecules
Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            789 TGGGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAGCT
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                                                                                                                                                                                                                                                                                                                                                                                            Score 157.2; DB 16;
Pred. No. 6.4e-39;
0; Mismatches 123;
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Pred. No. 3.7e-24;
0; Mismatches 70;
                                                                                                                                                                                                                                                                                               FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59138C.1
US-10-424-599-97591
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US-10-767-795-1320
APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecul TITLE OF INVENTION: Plants and Uses Thereof FILE REPERENCE: 38-21(53223)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 LENGTH: 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1320, Application US/10767795; Publication No. US20040181830A1; GENERAL INFORMATION:
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Best Local Similarity 69.5%;
Matches 166; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                              15.3%;
Similarity 65.3%;
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Best Local Similarity 65.3
Matches 231, Conservative
                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Glycine max
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USCUBLISHED NO. US20040009476A9

| Sequence 2973, Application US/09938842A
| Publication No. US20040009476A9
| Publication No. US20040009476A9
| GENERAL INPORMATION:
| APPLICANT: Harper, Jeff
| APPLICANT: Wang, Xun
| APPLICANT: Wang, Xun
| APPLICANT: Wang, Xun
| TITLE OF INVENTION: SAME, AND METHODS OF USE
| TITLE OF INVENTION: SAME, AND METHODS OF USE
| TITLE OF INVENTION: SAME, AND METHODS OF USE
| TITLE OF INVENTION: SAME, AND METHODS OF USE
| TITLE OF INVENTION: SAME, AND METHODS OF USE
| TITLE OF INVENTION: SAME, AND METHODS OF USE
| FILE REFERENCE: SCRIPIAGO 3
| FILE OF INVENTION UNMBER: US 60/227,866
| PRIOR APPLICATION NUMBER: US 60/227,866
| PRIOR PILING DATE: 2001-01-16
| PRIOR FILING DATE: 2001-01-16
| PRIOR FILING DATE: 2001-01-16
| PRIOR FILING DATE: 2001-06-22
| NUMBER OF SEQ ID NOS: 5379
| TOWN OF SEQ ID NOS: 5379
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Pred. No. 1.2e-20;
0; Mismatches 15; Indels
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9.8%; Score 101; DB 11; Length 20
Best Local Similarity 88.3%; Pred. No. 1.2e-20;
Matches 121; Conservative 0; Mismatches 15; Indels
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| PRIOR FILING DATE: 2000-08-24 | PRIOR APPLICATION NUMBER: US 60/264,647 | PRIOR PILING DATE: 2001-01-16 | PRIOR FILING DATE: 2001-01-16 | PRIOR FILING DATE: 2001-06-22 | NUMBER OF SEQ ID NOS: 5379 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO 2973 | SEQ ID NO
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Best Local Similarity 88.3%;
Matches 121; Conservative
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US-09-938-842A-2973
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Patent No. US20020160378A1
GENERAL INCOMPATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Traps, Joel
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REPRENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT PILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
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US-10-021-323-7926
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RESULT 15
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1 Sequence 3743, Application US/10739930

2 Fublication No. US20040216190A1

3 FUBLICATION INC. US20040216. David K.

3 APPLICANT: Kovalic, David K.

3 TITLE OF INVENTION: WCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

3 TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

4 TITLE OF INVENTION: US/10/739,930

5 CURRENT APPLICATION WUMBER: US/10/739,930

6 CURRENT FILING DATE: 2003-12-18

7 SEQ ID NO 3743

7 LENGTH: 2207
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                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Glycine max
PEATURE:
NAME/KEY: unsure
LOCATION: (1)..(2207)
OTHER INPORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER63260_1
US-10-739-930-3743
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L SUDMITTER (18-NOY-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jailnon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clept C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) : 5 prime and 3 prime are assembled with Phrap.
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Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menadd, M., Craudd, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana Full-length cDNA Complete sequence from clc GSLTFB50ZE05 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
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/mol_type="mRNA"
/strain="Col-0"
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HTC 06-FEB-2004

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Direct Submitseion

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage:
BP 191 91006 EWRX cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

Http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
                                                                                                                                                                                                         CNSOAGON
Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTIAS20ZG12 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
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CAAGGATGGTACGAATTCACTCTAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTTT 1034
                               Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Brantophyta; Uridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Location/Qualifiers
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/clone="GSLTLS20ZG12"
/tissue type="Adult vegetative tissue"
/plasmid="pcwySPORT 6"
complement(1. .1441)
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Pred. No. 1.6e-293;
0; Mismatches 1; I
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/organism="Arabidopsis thaliana"
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/strain="Col-0"
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Best Local Similarity 99.8%;
Matches 1025; Conservative C
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      /clone="GSLTFB50ZE05"
/tissue_type="Flowers and bu
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complement(1. .1307)
/gene="At3g18990"
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                          AGGGTCCCAGATAAGTTTGTGAGTAAATTCAAGGATGAGCTTTCGGTTGCTGTTGCACTC
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G. Genoscope members carried out sequencing and annotation: Castelli V., Aury J.M., Jailnoh O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIBS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length.
                                                                                                                                                                                                                                                                                                                             Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Location/Qualifiers
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/plamid="pc/WXPORT 6"
complement(1. .1375)
/gene="At3g18990"
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Pred. No. 1.8e-288;
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GSLTPGH54ZB04 of Hormone Treated Ca
Arabidopsis thaliana (thale cress)
                                                                                    BX824523.1 GI:42465662
HTC, GSLT. CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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/strain="Col-0"
/db_xref="taxon:3702"
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98.1%;
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524

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CNSOA6SO 1375 bp mRNA linear HTC 07-FEB-2004 Arabidopsis thaliana Full-length cDNA Complete sequence from clone

DEFINITION

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CNSOAD3Z

Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTPGH45ZCO5 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).
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    93, rue Henri accomplete 3 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Henri Rochefort 91025 BVRY CEDEX France
                                                                                                                                                                                                                                                                                                                                                                                             Score 470.8; DB 6;
Pred. No. 4.3e-130;
0; Mismatches 67;
                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="Jet Neuf"
/db xref="teaxon:3708"
/clone="BN25045C06"
/tissue type="seed"
/clone_lib="BN25"
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rosids, eurosids II, Brassicales, Brassicaceae; Brassica.
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EXELSES: I GI:42473387

HTC; GSLT cDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyea; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1490)
S Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
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Louditted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 1919 19106 EWRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads
Life Technologies (a division of Invitrogen) members carried out
full.length librairies construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.

Lotth, Www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
                                                                                           Eukaryotta; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 1420)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome
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42.9%; Score 441; DB 3; Length 1420;
Best Local Similarity 73.5%; Pred. No. 5.4e-121;
Matches 646; Conservative 0; Mismatches 195; Indels 38; Gaps
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/clone="GSLTPGH45ZC05"
/tissue type="Hormone Treated Callus"
/plasmid="pCwSPORT 6"
complement(1. .1420)
/gene="At1g49480"
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Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
WRGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                     http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
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/clone="GSLTPGH54ZB06"
/tissue_type="Hormone Try
/plasmid="pCMVSPORT 6"
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URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_BF/Full_length
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/clone="GSLTPGH132B06"
/tissue type="Hormone Treated Callus"
/plasmid="pCMVSPORT_6"
complement(1. .1490)
/gene="At1g49480"
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llarity 73.5%; Pred. No. 5.5e-121;
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Annotation Unpublished

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Lucited (18-NOV-2003) Genoscope - Centre National de Sequencage : Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weisenbach J., Salanoubat M.

UKGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque\_Projet\_EF/Full

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"
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/gene="At1g49480"

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AGCGTCTACATTTTCAATTTATCCCACTCTGAGATCAATTACCATTCCACGGGTCTCATG 330
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CGTTACTCCATTCGCATTGGTTATCTTTTGATTTTTAGATATGAAGGAAACTCTGCCTTC
                                                                                                                                           Arccrccacacrcrigagarcaaccacarrcragragrangercrrargcg----aarg
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                                                                                                                                                                                                                                             GATTCCGCACAGAATCAGTTCAACAAACGTCCTCGATTGTTTGAAGATCCTGAACTCAAA
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                                           CGTTTCTCCATTCGGATTGGT----TTCAGATACAAGTTACAGTCTACATTTTCAATTT
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BX841843.1 GI:42454500

HTC; GSLT_CDNA.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermacophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTLS76ZC03 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                        mRNA
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880 bp

CNS09Y69

RESULT 8 CNS09Y69 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

7; 210

Gaps

40;

Score 410; DB 3; Length 880; Pred. No. 9.9e-112;

39.9%;

Conservative

640;

151

Similarity

0; Mismatches 200; Indels

270

9

GGACTAAGGAAAGCTGACAACAAAATTTGGTTTCAAGATGGTTGGCAAGAGTTTGTTGAC

GGACTAAGGAAAGCCAACAACAAATCTGGTTTCAAGACGGTTGGCAGGAGTTTGTCAAC

116

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GTTCAAAGTTCTACGAGAGTGCTTCTGCGAAAAGAGAACCGTGACTGCAGAAGAAGAG
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 589)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of I2,028 non-redundant expressed sequence tags from normalized and blassicaelected cDNA libraries
DNA RES. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                AV540912.1 GI:8702670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Instituta
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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/clone="RZ157b09F"
/tissue_type="roots"
/clone_Tib="Arabidopsis_thaliana_roots_Columbia"
/note="Vector: pBluescriptII_SK-; Site_I: EcoRI; Site_2:
Xho!"
                                                                                                                                                                                                                                                                            685 GTGCCTCTACAAAGCAGGGAGAGCTAAGTTTAGCGAAGGATGGTATGAGTTCACACTCGA
                          565 ACCATCATATCTATACAGAGGTTGCATCATGTACTTGCCATCTGGGTTTGCTGAGAAATA
                                                                                                                                                                                                                           625 CCTAAGTGGGATATCTGGTTTCATCAAGCTCCAGCTCGGTGAGAAACAATGGCCAGTGAG
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CCTAATCCCGAGGAAGTAAACTCTTCAACTCCCGGTGGAGATGACTCAGAGAACCGCTCA
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Pred. No. 2.5e-109;
0; Mismatches 2;
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/mol_type="mRNA"
/ecotype="Columbia"
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99.5%;
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Best Local Similarity 99.5
Matches 403; Conservative
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryotz, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 780)
Seliner; T., Immink, R.G.H., Cahill, D.J. and Kersten, B.
Generation of a cDNA expression library from Arabidopsis inflorescence meristem
L Unpublished (2003)
Contact: Birgit Kersten
Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Inhestr: 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131128
Email: Kerstena@molgen.mpg.de
Insert Length: 780 Std Error: 0.00
Plate: 204 row: O column: 14
Seq primer: posts.
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/ecotype="Columbia"
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/db_xref="taxon:3702"
/clone="MPMGp2011014204"
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/note="Vector: pQE-30NAST-attB (AY386205); Site_1: SalI;
/site_2: Not1; About 1 week after bolting, cDNA synthesis
using SuperscriptTM-system (Invitrogen) with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               780 bp mRNA linear EST 01-JUN-2004
204014.pl AtMl Arabidopsis thaliana cDNA clone MPMGp2011014204
CK120978
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TAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTGTTTTGAGCTGCTCAGAACCAGAGATT
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1. 780
/organism="Arabidopsis thaliana"
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GI:5843380
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oligo(dT)-primer containing NotI restriction site and a SaII adapter. The main library (plate numbers begin with 1) of 38,000 clones was rearrayed into the sublibrary (plate numbers begin with 201) containing 5,000 putative expression clones. Average insert size is 1 kb. Note: The rearrayed sublibrary (plate numbers begin with 201) was sequenced. Library generation and sequencing was granted in context of GABI-LAPP; data are also accessible at https://gabi.rzpd.de"
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                                                                                                                                                                                                                                                                                                                       CATTCGGATTGGT----TICAGATACAAGTTACAGTCTACATTTTCAATTTATCCTCCA 116
                                                                                                                                                                                                                                                                                                                                                                                  CACTCTGAGATCAACCACC---ATTCTAGTGAAGCTCTTATGCAAATGGATTCCGC 172
                                                                                                                                                                                                                                                                                                                                                                                                                339 TCACAACCACTT---CAAACGCGCCCGTTTGTTTGAAGACCTTGAAGATGAAGATGCCGA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCAGCCAAAACGTTCGAACCAACAAACCCTTTCTTCAGAGTGGTTCTGCGACCATCCTA 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      626 GATATCTGGTTTCATCAAGCTCCAGCTCGGTGAGAACAATGGCCAGTGAGGTGCCTCTA 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAAGCAGGGAGAGCTAAGTTTAGCCAAGGATGCTATGAGTTCACACTCGAGAACAATAT 745
                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                         219 CATTCGCATTGGTTATCTTTTGATTTTTAGATATGAAGGAAACTCTGCCTTCAGCGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456 CAAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCACTGGACCAGTTAAAGCTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                516 GCCAACGCCAACCCCAAAATACCTAAAAAGAGAGGAGGAAGAAGAAAAATGCTGATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576 TGAGGAAATAAACTCATCAGCTCCGCGAGATGATGATCCAGAGAACCGTTCAAAGTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAAGCCAACAACAAAATCTGGTTTCAAGACGGTTGGCAGGAGTTTGTCAACCGTTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTCATTTATC---------CATCGAACCCTGAATCTACTGAACCAGTGAA
                                                                                                                                                                                                                             GAAAGCTGACAACAAAATTTGGTTTCAAGATGGTTGGCAAGAGTTTGTTGACCGTTACTC
                                                                                                                                                                                                                                                                                                                                                     CATITICAATITIATCCCACTCTGAGATCAATTACCATTCCACCGGTCTCATGGATTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 TAAAGGTTATGGCGGTTCTACAGCCATCCAAAGCTTTTTCAAAGAATCTAAAGCTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386 CGAGGAAGTAAACTCTTCAACTCCCGGTGGAGATGACTCAGAGAACCGCTCAAAGTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTATACAGAGGTTGCATCATGTATCTTCCTTCTGGGTTTTGCTGAGAAGTACCTAAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCATCTTTCCTTCTGTGTACCCATCACCACTTCCTGAGTCTACAGTACCAGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recasccaaacarrcsaaccaacaarccrracrrrasacrrsrrsrscsaccarcara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCTCCGGGTTCATCAAAGTCCAGCTTGCGGAGAAACAATGGCCTGTTCGATGTCTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAAGCCGGGAGGCCAAATTCAGTCAAGGATGGTACGAATTCACTCTAGAGAACAACTT
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                  38;
                                                                                                                                                                      Length 780;
                                                                                                                                                                                                  Indels
                                                                                                                                                                   Score 396.2; DB 7;
Pred. No. 1.4e-107;
0; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGAGAAGGACGTCTGTGTGTTTGAGCTGCTCA
                                                                                                                                                                   Query Match 38.6%;
Best Local Similarity 72.9%;
Matches 594; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206
                                                                                                                                                                                                                                159
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/tissue_type="root"
/dev_stage="4 - 7 weeks"
/dev_stage="4 - 7 weeks"
/dev_stage="4 - 7 weeks"
/clone_lib="A. thaliana, Columbia Col-0, root-1"
/note="Voctor: pSPORT; Site_1: Not1; Site_2: Sal1; cDNA
library was derived from untreated root tissue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1:1:1 peat moss/vermiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with fertilizer. cDNA synthesis was initiated
using a Not1-oligo(dT) primer. Double-stranded cDNA was
blunted, ligated to Sal1 adaptors, digested with Not1,
size-selected, and cloned into the Not1 and Sal1 sites of
AI996485 51 bp mRNA linear BST 08-SEP-1999 701666887 A. thaliana, Columbia Col-0, root-1 Arabidopsis thaliana CDNA clone 701666887, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                 Gilliland, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533
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                                                                                                                                                                                                                           Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAGCTTGCGGAGAAACAAT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGTCAAGGATGGTACGAAT 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCAACAAAACCCTTTCTTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 591)
Chen,J., Momiyama,M., Chan,B., Mooney,M., Carroon,B., Gillilanc Wang,X., Hillman,J., Guegler,K., Kim,C., Doyle,M., Brzoska,P., Gorgone,G., Burns,D., Griffin,J., Mouanoutoua,M., Nguyen,D., Tan,R., Rose,M., Warren,B., Ton,B., Kastury,K., Borillo,C., Carpio,T., Policky,J., Suzuki,G., Argentine,C., Shah,S., Nobriga,A., Murry,L., Turner,C., Krikorian,S., Elder,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   591 GAACCGTTCAAAGTTC-ACGAGAGTGCTTCTGCGAGAAAGAGAACCGTTGACTGCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGAGAGAGCCATCAATGCAGCCAAAACGTTCGAACCAACAAACCCTTTCTTCAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
Pharmaceuticals, Inc.
Fast 3 World Parkway Circle, St. Louis, MO 63134, USA
Tel: 877-577-273
Fax: 314-427-3324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson, D.
Arabidopsis thaliana Gene Expression MicroArray
Unpublished (1999)
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    .591
    /organism="Arabidopsis thaliana"

                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: service@genomesystems.com
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="701666887"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 857
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CD823066
BN25.047120F020109 BN25 Brassica napus CDNA clone BN25047120, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Varidiplophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 645)
                                                                                                                                                                                                                                                                                                                                                                            586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525 TIGCIGAGAAATACCTAAGTGGGATATCTGGTTTCATCAGGTCCCGGTGGGGAAAC 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGTCAAGGATGGTACG 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     914 AATTCACTCTAGAGAACAACTTAGGAGAGAGGACGTCTGTGTGTTTGAGCTGCTCAGAA 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant genomics programme 'Genoplante' (http://www.genoplante.comand http://genoplante-info.infoblogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence has been generated in the framework of the french
                                                                                                                                                                                                                                                                                                                                                                        645 AGGAAAGAGAGAGCCGTCAATGCAGCCAAAACATTCGAACCAACAAATCCTTACTTTA
                                                                                                                                                                                                                  674 AAGAAAGAGAGAGAGAGATGAATGCAGGCAAAAAGGTTGGAACCAAAAAAAGCTTTCTTCA
                                                                                                                                CAGAGAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAACCGTGACTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGTGGTTCTGCGACCATCCTATACAGAGGTTGCATCATGTATCTTCCTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585 GAGTTGTTGTGCGACCATCATATCTATACAGAGGTTGCATCATGTACTTGCCATCTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTCCAGCTTGCGGAGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    974 CCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTACGTCTGA 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293
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Pred. No. 8.5e-103;
0; Mismatches 53; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Denote the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state o
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/clone="BN25047120"
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/cultivar="Jet Neuf"
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Best Local Similarity 88.6%;
Matches 412; Conservative
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Brassica napus
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Genoscope - Centre National de Sequencage

BP 191 91006 ENTRY cedex - France

BP 191 91006 ENTRY cedex - France

Email: sequescope.ons.fr, Web : www.genoscope.cns.fr

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out

Life Technologies (a division of Invitrogen) members carried out

full-length librairies construction: Temple G.

Genoscope members carried out sequencing and annotation: Castelli

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.

URGV INRA: Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis

genome released by MIPS (Wunich Information center for Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Craud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Pull-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 CTGAGTCTACAGTACCAGCCAACAAGGGTATGCTAGTTCAGCCATCCAAACCTTGTTCA 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX835682 Arabidopsis thallana Adult vegetative tissue Col-0
BX835682 Arabidopsis thallana Adult vegetative tissue Col-0
Arabidopsis thallana cDNA clone GSLTLS48ZH11 3PRIM, mRNA sequence-
BX835682
BX835682.1 GI:42529765
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/clone lib="Arabidopsis thaliana Adult vegetative tissue
Col-0"
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                                                                                                                                                                                    292 TCACTCTAGAGAACAACTTAGGAGAAGGAGACGTCTGTGTGTTTTGAGCTGCTCAGAACCA
                              GGCCTGTTCGATGTCTACAAAGCCGGGAGAGCCAAATTCAGTCAAGGATGGTACGAAT
                                                                                                               TCACTCTAGAGAACATTAGGAGAAGACGTCTGTGTGTTTGAGCTGCTCAGAACCA
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                                                                                                                                                                                                                                                                              977 GAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTACGTCTGAA 1027
                                                                                                                                                                                                                                                                                                                         232 GAGATTTCGTTTTGAAAGTGACAGCCTTTCGAGTCAACGAGTACGTCTGAA 182
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Pred. No. 1.9e-103;
0; Mismatches 114;
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/mol type="mRNA"
/ectype="col-0"
/db_xref="taxon:3702"
/clone="GSLTLS48ZH11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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llarity 79.3%;
Conservative
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Unpublished (2004)
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Best Local S:
Matches 470
                                                                                                                        917
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
BX835682/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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AUTHORS
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ORIGIN  Query Match 35.3%; Score 362.6; DB 7; Length 906; Best Local Similarity 64.8%; Pred. No. 1.9e-97; Matches 587; Conservative 0; Mismatches 310; Indels 9; Gaps 3;  Qy 24 GTTGATTTTCATCCACTATCCAAGAAAACGTCTGAGGGTCCCAGATAAGTTTGTGAG 83	Db 1 GCTTATTCTCTCCCCCCCCCAAGAAAAAATTGAACTGAACTGATCCCTGATAACTTCGTTAA 60  Qy 84 TAAATTCAAGGATGAGCTTTCGGTTGCTGTTGCACTCACAGTACCTGATGGTCATGTTTG 143	144 GCGTGTAGGAAGGTGACAACAAAATTTGGTTTCAAGATGGTTGGCAAGAGTT	204 TGTTGACCGTTACTCCATTCGCTTATCTTTTGATTTTTAGATATGAAGGAACTC 181 TCTAGAGCGTTACTTTCGTGTTGGCTACGTATTTGGTTTTTAGATACGAAGGAAATTC	264	Qy 324 TCTCATGGATTCCGCTCACAACACCACTTCAAACGCGCCGTTTGTTT	361 TGAATGCATCTCCAGCACTTCAGAATTTGTTGGTGGGTCTAAACTTAACAACTGCAT	Qy 444 AGTACCAGCCAACAAAGGGTATGGTAGTTCAGCCATCCAAACCTTGTTCACTGGACC 500	Oy 501 AGTTABAGCTGAAGGCCAACGCCAAAATACCTAAAAAGAGAGGAGGAA 557	Qy         558         GAAGAAAATGCTGATCCTGAGAAATAAACTCATCAGCTCCGCGAGATGATGATCCAGA         617           Db         541         AAAGCGGAAGTTTGATCCTAACGTGCAGGATTCATCTGCTGGAGGTGAAGATGATGATGA         600	QY         618 GAACCGTTCAAAGTTCTACGAGAGTGCTTCTGCGAGAAAGAGAAACGTGACTGCAGAAGA 677           DD         601 TATGCGCTTTAGAAGTGCTTATGAAAGTGCTTCAGCCCGAAACAGAACCGTGACACCTGAAGA         660	678 AAGAGAGGCCATCAATGCAGCCAAACGTTCGAACAACAACCAAC	Qy 738 GGTTCTGCGACCATCCTATACAGAGGTTGCATCATGTATCTTCCTTC	Oy 798 TGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAAGTGCGGAGAAACA 854	855	Qy 915 ATTCAC 920	501 MILLO 50 SULT 15 813712
	CTTCTC	791 GGTTTGCTGAGAAGTACCTAAGTGGGATCTCCGGGTTCATCAAGATCCAGCTTGCGGAGA 	QY     851     AACAATGGCCTGTTCGATGTCTCTACAAAGCCGGGAGAGCCAAATTCAGTCAAGGATGGT     910       Db     301     AACAGTGGCCGGTGAGATGCCTTTACAAAGCAGGAGAGCCAAGTTCAGCCAAGGGTGGT     360	QY         911 ACGAATTCACTCTAGAGAACTAGGAGAAGGAGACGTCTGTGTGTTTGAGCTGCTCA 970           Db         361 ACGAGTTCACCTGGAGAACAACTAGGAGAAGGTGACGTCTGCGTGTTCGAGCTCCCTCA 420	Oy 971 GAACCAGAGATTTCGTTTTGAAAGTGACAGCCTTTCCAGTCAACG 1015 	RESULT 14	_	ACESSION COIO8220.1 GI:48806906 KEYWORDS EST. SOURCE GOSSYPium raimondii	E	RS CB	TITLE Global assembly of Cotton ESTs JOURNAL Unpublished (2004) COMMENT Contact: Rod A. Wing Arizona Genomics Institute	The University of Arizona Forbes Building Room 303, Tucson, AZ, 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259	Email: http://genome.arizona.edu Plate: 0039 row: N column: 17. FEATURES Location/Qualifiers BOUTCE 1. 906	/organism="Gossypium raimondii" /mol_type="mRype" /db_xref="taxon:29730" /clone="GR_Ebo039N17"	/tissue_type="floral" /dev_stage=" 3 to +3 DPA" /lab_host="DHDBB" /rlone_lih="GP_Ph"	/ John July Carlo John Sport 6.1; Site 1: Not1; Site 2:     ECORV; Library made by Invitrogen with RNA supplied by Wendle lab. Directional cloned into Not1-EV. Colonies plated/picked by AGI. More glycerol clones held in -80."

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EST 10-JUL-2003
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612 bp mRNA linear EST 10-JUL-200.
BN15.020L13F020211 BN15 Brassica napus cDNA clone BN15020L13, mRNA
sequence.
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Contact: Genoplante
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6anoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
7el: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Fax: 33 1 69 47 56 00
plant genomics programme 'Genoplante' (http://www.genoplante.complant genomics programme 'Genoplante' (http://www.genoplante.complant floation/Qualifiers
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/clone="RN15020113"
/tissue_type="seed"
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KEYWORDS
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ORGANISM
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AUTHORS
TITLE
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Compugen Ltd
version :
GenCore (c) 1993
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- protein search, using sw model OM protein

December 29, 2004, 13:02:12 ; Search time 98 Seconds (without alignments) 2002.069 Million cell updates/sec Run on:

US-10-088-187A-11 1796 Title: Perfect score:

1 MPRPFFHKLIFSSTIQEKRL......LLRTRDFVLKVTAFRVNEYV 341 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 segs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Bed Bed 88 Minimum I Maximum I

length: 0 length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Q813w1 arabidopsis	Q6r2u8 brassica ca	Aar92199 brassica	Q6v0j6 brassica ca	Aaq55453 brassica	Q91j67 arabidopsis			Q8s2e6 oryza sativ	Q851v0 oryza sativ		Q8ryd1 arabidopsis	Q9zsh7 arabidopsis	N	Q9sza5 arabidopsis	Q91j70 arabidopsis	Q84r27 arabidopsis		Q9fjg2 arabidopsis			Q9fgd2 arabidopsis			Q91sp6 arabidopsis	Q84re8 arabidopsis			Q9sz05 arabidopsis	Q6z0d2 oryza sativ	Bad03253 oryza sat
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d	Query	Match	100.0	84.2	84.2	84.0	84.0	9.99	52.7	52.4	15.5	•	13.7	13.3	12.8	12.8	12.7	12.2	12.0	11.9	11.3	11.0	10.9	10.7	10.6	10.2	10.0	9.9	9.8	9.6	9.6	9.5	9.5
		Score	1796	1513	1513	1509	1509	1197	946	942	278	251.5	246	239	229	229	227.5	219.5	215.5	214	203	197	195.5	192	191	182.5	179.5	177.5	175.5	172	172	170.5	170.5
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## ALIGNMENTS

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PQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFRRA 120
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MEDLINE=22111275; PubMed=12114624;
MEDLINE=22111275; PubMed=12114624;
Levy Y.Y. Mesnage S., Mylne J.S., Gendall A.R., Dean C.;
Levy Y.Y. Mesnage S., Mylne J.S., Gendall A.R., Dean C.;
Levy Y.Y. Mesnage S., Mylne J.S., Gendall A.R., Dean C.;
Lime control., 1.

Science 297:243-246 (2002).

REMBL; AF289051; AAN76972.1; -.

REMBL; AF289051; AAN76973.1; -.

ROJ GO:0003677; F:DNA binding; IEA.

GO; GO:0003677; F:DNA binding; IEA.

ROJ GO:0005555; P:regulation of transcription, DNA-dependent; IEA.

ROJ GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

REMBL; PROSITE; PS09863; B3; 2.

REMSL; REMSL; PS09863; B3; 2.

REMSL; REMSL; REMSL; PS09863; B3; 2.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
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                                                                                                                                           (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                           341 AA
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Matches 341; Conservative
                                                                           PRELIMINARY;
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Matches 296; Conservative
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                  STRAIN=cv. Kwonsim;
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SEQUENCE FROM N.A.
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NCBI_TaxID=3711;
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02-MAR-2004 (TrENBLrel. 27, Created)
02-MAR-2004 (TrENBLrel. 27, Last sequence update)
02-MAR-2004 (TrENBLrel. 27, Last sequence update)
Reduced vernalization response 1.
Brassica campestris (Field mustard).
Brassica campestris (Field mustard).
Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
NCBL_TAXID=3711;
                                                                                                                                                                                                                                             Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
NCBI_TAXID=3711;
                                                                                                                                                                                                                                                                                                                                                     Kim J.-S.,
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Kwon S.-J., Park B.-S., Kim S.-Y., Choi H.-S., Lee M.-C., Kim Lee S.-I., Lim K.-B., Kim J.-A., Lee M.-R., Jin Y.-M., Kim D., Kim H.-I., Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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84.2%; Score 1513; DB 2; Length 329;
Best Local Similarity 85.1%; Pred. No. 1e-107;
Matches 296; Conservative 13; Mismatches 13; Indels 2
                  38058 MW; A24ADB91433459BB CRC64;
                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Reduced vernalization response 1.
Brassica campestris (Field mustard).
OGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV
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InterPro; IPR003340; TF_B3.
Pfam; PF02342; B3; 2.
PROSITE: PSG683; B3; 2.
SEQUENCE 329 AA; 38058 MW
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EMBL, AN356368, AAQ55453.1; -.

InterPro; IPR00340; TF_B3.

PROSITE; PS50863; B3; 2.

SEQUENCE 329 AA; 37931 MW; BFF71D55ADE2655A CRC64;
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Kwon S.-J., Park B.-S., Kim S.-Y., Choi H.-S., Lee M.-C., Kim J.-S.,
Lee S.-I., Lim K.-B., Kim J.-A., Lee M.-R., Jin Y.-M., Kim D.,
Kim H.-I.;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Reduced vernalization response 1.

Brassica campestris (Field mustard).

Bussyota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; endicoryledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                    Length
                                                                                             "Brassica rapa Kwonsim VRN1 mRNA.";
Submitted (DEC-2203) to the EMBL/GenBank/DDBJ databases
EMBL; AYS17929; AAR931199.1; -
SEQUENCE 329 AA; 38058 MW; A24ADB91433459BB CRC64;
                                                                                                                                                                                                                                             Query Match

84.2%; Score 1513; DB 2;
Best Local Similarity 85.1%; Pred. No. 1e-107;
Matches 296; Conservative 13; Mismatches 13;
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85.1%; Pred. No. 2e-107;
ive 12; Mismatches 14;
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                                          FKRARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEE--PT 174
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                                                                       PTPKI PKKRGRKKKNAD-PEEINSSAPRDDDPENRSKFYESASARKRTVTAEERERAINA 233
                                                                                                                                                      AKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAEKQWPVRCLYK 293
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                                                                                                                                                                       222 AKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLGEKQWPVRCLYK
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                          AGRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV 341
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85.1%; Pred. No. 2e-107;
ive 12; Mismatches 14; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AY356368; AAQ55453.1; -. SEQUENCE 329 AA; 37931 MW; BFF71D55ADE2655A CRC64;
                                                                                                                                                                                                                                                                                                                                             02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
CP-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Reduced vernalization response 1.
Brassica campestris (Field mustard)
                                                               02-MAR-2004 (TrEMBLrel. 27, Created)
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Matches 296, Conservative
                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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AAQ55453;
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                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AP000735; BAB01695.1; -.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006357; P:DNA binding; IEA.
GO; GO:0006357; P:PNA binding; IEA.
FIREM: PPCO: IPR003340; TF_B3.
FEAM: PPC03182; B3: 1.
FROSITE; PS50863; B3: 1.
SEQUENCE 230 AA; 26219 MW; B96A826B384C9F3C CRC64;
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Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altafi H., Araujo R., Huizar L., Rowley D., Buehler B., Dunn P.,
Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
Iuros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
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Pred. No. 1e-83;
0; Mismatches
230 AA
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                                                                                       Created)
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99.1%;
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PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
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As Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Rasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y., Rasaki T., Matsukawa M., Arikawa K., Chiden Y., Hayashi M., Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M., Ramoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C., Rasaswa W., Kataga M., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K., Rasaswa W., Katagari S., Kikuta A., Kobayashi N., Kono I., Machita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Sugasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., Song U., Takazaki Y., Terasawa K., Tsuji K., Aninckawa T., Shomura A., Song U., Takazaki Y., Terasawa K., Tsuji K., Aninckawa T., Shomura A., Song U., Takazaki Y., Terasawa K., Tsuji K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., Ann M., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Anne Genome sequence and structure of rice chromosome I.";

Namiki A., Namagata H., Shabata M., Ramara H., Yoshiki S., Yoshihara R., Yukawa K., Tarasawa K., Turke Genome sequence and structure of rice chromosome I.";

Namiki A., Namagata H., Pata M., Namiki K., Walana H., Ilan M.Y., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namiki M., Namik
TVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPK------KRGRKKKKNADPEEIN- 196
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192 TAVKNEEDADE----LPVCELPASSASPPRHVPEGALDADGGAARRGAAKTRSLQDDLAL 247
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                                                                                                   228 ERAINAAKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAEKQWP
                                                                                                                                                                                                                              288 VRCLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last anno
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Submitted (Unn-201) to the EMBL/GenBank/DDBJ databases.
EmBL; AY043868; AAK68808, 1; -600, GO:0003677; F:DNA binding; IEA.

GO: GO:00036355; P:regulation of transcription, DNA-dependent; IEA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F13F21.8;
Name=F13F21.8;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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      Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
Brabi, ACO07504, AD43153.1; -.
PIRI, E95531, E95531.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                            18; Indels
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                                                                                                                                                                                                                                                                                                    226 AA; 25850 MW; CB902C811E446A67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   52.7%; Score 946; DB 2;
81.2%; Pred. No. 1.7e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
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Matches 189; Conservative 13; Mismatches
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Matches 190; Conservative
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PROSITE; PS50863; B3;
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                                                          81 IFRYEG-NSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKRARLFEDLEDE-DAEVIFPSS 138
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 SSAPRDDDPENRSKFYESASARKRTVTAEERERAINAAKTFEPTNPFFRVVLRPSYLYRG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 VYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPK--KRG------RKKKN 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRPSYL--YRGCIMYLPSGFAEKYLSGISGFIKVQLAEK--QWPVRCLYKAG-RAKFSQG 302
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             CIMYLPSGFAEKYL-SGISGFIKVQLAEKQWPVRCLYKAG-RAKFSQGWYEFTLENNLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    582 GEDEDVVAAA----EGGRYGEYYFSRHGRVABYNLREEDREEISRVPVPVQPGNPVFVQV
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                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantes, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Wang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salberg S.L., Fraser C.M.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0003677; P:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00340; TF_B3.
Pfam; PF02362; B3; 4.
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Last annotation update)
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                                                                                                       GDVCVPELLRTRDFVLKVTAFRVNE 339
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01-WAR-2004 (TREMBLrel. 26, Last
Putative auxin response factor.
Name=OSJNBD0111B07.22;
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Gramene; Q851V0; -.
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hes 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIDNCNKKMKTEHASSSEDDQ-----ETPTAEVHRMKVEEMVRAIHS-----NHPV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRVVLRPSYLYR-GCIMYLPSGFAEKYLSGISGFIKVQLAEKQWPVR-CLYKAGRAKFSQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 WAEFANSHDIKMGDFLVFRYTGNSQFEVKIFDPS-----GCVKAASHNAVNIGQHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 QNMQGDPIEILSCSDEHLRAQSLTTERQNQ--------PEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PFHKLIPSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWFQDG
                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II.L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Wang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salberg S.L., Fraser C.M.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 246; DB 2; Length 10;
; Pred. No. 5.9e-10;
60; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Buell R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                  24, Last sequence update) 25, Last annotation update)
                                                                                                                                                  1029 AA.
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                                                                                                                                                                                             Created)
                                                                                                                                                  PRT;
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Name=OSJNBb0111B07.17;
303 WYEFTLENNLGEGDVCVFEL
                      | :| :| | ||:|||
698 WRQFAGDNRLVAHDVCLPEL
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23.8%;
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Beet Local Similarity 23.00,
Conservative /
                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                        (TrEMBLrel.
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GWRKFTRDNEL
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QBRYD1
ID QBRYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 FGWDKFVKDHSLEENDLLVFKFHGVSEFEVLVFDGQTLCEKPTSYFVRKCGHAEKTKASH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 HNHFKRARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 AINAAK-TFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAEKQWPV 288
                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                  31 PGFH------NRLVIPRKFSTHCKRKCLPQIVTLKSPSGVTYNVGVEEDDEKTMAFR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KADVEMISAGSNKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 TPTPKIP----KKRGRKKKNADPEEINSSAPRDDDFENRSKFYESASARKRTVTAEERER
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 RC-LYKA-GRAKFSQGWYEFTLENNLGEGDVCVFELL--RTRDFVLKVTAFRVNE 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Name=T15B16.18 protein (Hypotherical protein AT4901580).
Name=T15B16.18; Synonyms=AT4901580;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids:
eurosids II; Brassicales; Brasslacaeae; Arabidopsis.
                                                                                                                                                                                                                                  EMBL, AJ441117; CAD29616.1; -.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA
                                                                                                                                                                                                                                                                                                                                                                                 82;
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                                                                                                                                                                          SEQUENCE FROM N.A.
Sessa G., Carabelli M., Ciarbelli A.R., Ruzza V., Steindler
                                                                                                                                                                                                                                                                                                                                                       Length 337;
                                                                                                                                                                                                                                                                                                                                                   Query Match
13.3%; Score 239; DB 2; Length 33
Best Local Similarity 24.5%; Pred. No. 4.5e-10;
Matches 87; Conservative 57; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                           Sessa G., Carabelli M., Ciarbelli A.R., Ruzza V., Steinc
Ruberti I.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                             InterPro; IPR003340; TF_B3.
Pfam; PP02362; B3; 2.
PROSITE; PS50863; B3; 2.
SEQUENCE 337 AA; 38760 MW; 8CA7E445600DA3CB CRC64;
             (TrEMBLrel. 21, Created)
(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 TGYEQEEHINSDIDTASAQL------PVISPTSTVRVSEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KYPLSGFKKMRRELSNDNLDQ-
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                                                        Auxin response factor 36.
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                                                                                                                                              NCBI_TaxID=3702;
               01-JUN-2002
01-JUN-2002
                                          01-OCT-2003
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SEQUENCE FROM N.A.

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30 PPKLVLPSTWKDKMMRIPPRFVKLQGSKLSEVVTLVTPAGYKRSIKLKRIGEBIWFHEGW
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Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledoms; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledoms; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                          Cheuk R., Chen H., Kim C.J., Shinn P., Carninci P., Hayashizaki Y., Chan B., Kawai J., Narusaka M., Sakurai T., Satou M., Seki M., Shinozaki K., Ecker J.R., R., Shinozaki K., Ecker J.R., Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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"Arabidopals ORP clones.";
"Arabidopals ORP clones.";
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BT01064, AA089626.1;
ERBL; BT01064, AA089626.1;
SEQUENCE 190 AA; 22122 MW; D7FB2C343E4BC915 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; T02015; T02015.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:00036355; P:regulation of transcription, DNA-dependent;
InterPro; IPR008932; Cupredoxin.
InterPro; IPR003340; TF_B3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [5]
SEQUENCE FROM N.A.
Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104919; ARC72857.1; -.
EMBL; BT010604; AAQ898526.1; -.
EMBL; AL161492; CAB77728.1; -.
                                      the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
12.8%; Score 229; DB 2;
Best Local Similarity 33.3%; Pred. No. 1.2e-09;
Matches 53; Conservative 25; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 AA.
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(NOV-1998)
T., Smith F
(NOV-1998)
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AAQ89626;
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AAQ8

AAQ8

AAQ8

DT AQ2-W

DT 02-W

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01-MAY-2000 (TERMBLrel. 13, Last sequence update)
01-MAY-2000 (TERMBLrel. 27, Last annotation update)
Hypothetical protein F17MS.40 (Hypothetical protein AT4g33280).
Name=F17MS.40; Synonyme=AT4g33280;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALIG15678; CAB30786.1; -..
EMBL; ALIG1583; CAB80045.1; -..
GO; GO:0003677; P:DNB binding; IEA.
GO; GO:0003577; P:PNB binding; IEA.
GO; GO:0005357; P:PNB binding; IEA.
Hypothetical protein.
Hypothetical protein.
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                            Length 190;
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                      ch 12.8%; Score 229; DB 2; Similarity 33.3%; Pred. No. 1.2e-09; 53; Conservative 25; Mismatches 51
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Best Local Similarity
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THIS PAGE BLAWK (USPID)

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5.1.6
Compugen Ltd.
version :
GenCore (c) 1993
       Copyright
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OM protein - protein search, using sw model

December 29, 2004, 19:00:56; Search time 23 Seconds (without alignments) 1426.518 Million cell updates/sec Run on:

US-10-088-187A-11 1796 I MPRPFFHKLIFSSTIQEKRL......LLRTRDFVLKVTAFRVNEYV 341 score: Title: Perfect f

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: "Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\* Database :

piri:\* pir2:\* pir3:\* . . . .

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	Н	_		_	_	_	_	_				hypothetical prote	⊣	hypothetical prote				_		hypothetical prote	o	reproductive meris	F19K19.7 protein -	hypothetical prote		hypothetical prote	o	homeobox protein c
SUMMARIES				_	_	~				_	_	_	••	_	~	•	•		01	•	_	~	•	~	_		•	_	_	_
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	Query Match Length	226	190	461	308	286	389	352	344	210	283	461	490	512	984	1440	899	493	478	851	608	1021	2783	497	134	232	243	482	1507	298
ď	Query Match	52.7	12.8	12.7	10.2	9.6	9.6	9.0	8.1	7.9	7.9	7.8	7.7	7.5	7.4	7.4	7.4	7.3	9.9	6.5	6.2	6.2	6.0	5.8	5.7	5.7	5.7	5.7	5.6	5.5
	Score	946	229	227.5	182.5	172	172	161.5	145	141.5	141	140.5	137.5	~	ë.	133.5	133	132	118	116.5	111	110.5	107.5	104	102.5	102.5	101.5	101.5	101	66
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hypothetical prote	hypothetical prote	hypothetical prote	TonB protein [impo	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	MG032 homolog B01	hypothetical prote	hypothetical prote	translation elonga	hypothetical prote	probable secreted	hypothetical prote	heat shock protein
T29657	T26819	T15269	AD0267	T05109	A84767	T06310	G96511	S73444	T45894	T16740	S38003	T00948	C81357	G84639	T09882
7	~	~	N	7	~	N	N	-	N	N	N	N	N	N	N
586	720	1082	252	525	297	852	616	673	932	1003	1008	599	541	682	823
5.5	5.5	5.4	5.4	5.4	5.4	5.3	5.3	5.3	5.3	5.3	5.2	2.5	5.1	5.1	5.1
86	98	97.5	97	97	96.5	96	95.5	95	95	94.5	94	92.5	92	92	95
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## ALIGNMENTS

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Paperhetical protein F13F21.8 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: E56531
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunder, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J. M.F.; Li, Y.; Lin, X.; Lin, S.X.; Liu, Z.A.; Lurce, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.K.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Status: preliminary
A;Status: preliminary
A;Reacterne type: DNA
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A;Residues: 1-226 <STO> A;Cross-references: UNIPROT:Q9XIB5; GB:AE005173; NID:g5430753; PIDN:AAD43153.1; GSPDB:GR C;Genetics:

A; Map position: 1

Gaps 12; 52.7%; Score 946; DB 2; Length 226; 81.2%; Pred. No. 3.3e-69; ive 14; Mismatches 18; Indels Best Local Similarity 81.2\* Matches 190; Conservative Query Match Best Local Similarity

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110 MDSAHNHF-KRARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGY-ASSAIQTLFTGP 167 m à 셤

227 168 VKAEEPTPTPKIPKKRGRKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEER à

56 SKAEE---TPKVLKKRGKKKKNPNPEEVNSSTPGGDDSENRSKFYESASARKRTVTAEER 112 셤

ERAINAAKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAEKQWP 287 228 δ

113

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VRCLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV 341 288 173 ò a

RESULT ;

hypothetical protein T15B16.18 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 09-Jul-2004

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49920
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24490
A;Accession: T49920
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C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C'SACCESSION: H84537
R'in, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R'in, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: UNIPROT:091XE1; EMBL:AL353994; GSPDB:GN00063; ATSP:F17114.30
A,Experimental source: cultivar Columbia; BAC clone F17114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
              328 AGSNKKALSL-----AKRAISPDG--FLVFMKRSHVVSKCFLTIPYKWCVKNMLITR 377
                                                                                                    275 GFIKVQLAEKOWPVRC-LYXA-GRAKFSQGWYEFTLENNLGEGDVCVFELL--RTRDFVL 330
                                                                                                                                    64 --GWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKRAR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 KSGWEKFVIDNALGDHEFLIFTHKGQMSFTVKIFNKDGKEMMQPPQSRASFASS--SRVK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 LFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 KRGRKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEERBRAINAAKTF--EP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 TNPF--FRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQL--AEKQWPVRCLYKAG 295
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213 SSSVAGFKIFISKSYIKS---LAIPKPFG-NYMPKEKTRVKIHHPDGEKTWKVVFVVKER 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.2%; Score 182.5; DB 2; Length 308; Best Local Similarity 24.6%; Pred. No. 3.1e-07; Matches 83; Conservative 51; Mismatches 145; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 33/3; 132/1; 231/3
C;Superfamily: Arabidopsis thaliana hypothetical protein F17114.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 RAKFSOGWYEFTLENNLGEGDVCVFELLRTRDFVLKVT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 GQIFSGGWKRLCKEYPVVFGDTCKFTLITPLELLLVVS 306
                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F17I14.30 - Arabidopsis thallana
                                                                                                                                                                                                                                                                            438 NVYIFRGEE 446
                                                                                                                                                                                                                    331 KVTAFRVNE 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-308 <BEV>
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Typothetical protein F17M5.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1399 #sequence_revision 30-Apr-1399 #text_change 09-Jul-2004
C;Accession: T05979
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15263
A;Rosesion: T05979
A;Molecule type: DNA
A;Residues: 1-461 - 8EEV>
A;Cross-references: UNIPROT:Q98ZA5; EMBL:AL035678; GSPDB:GN00062; ATSP:F17M5.40
A;Experience and source: cultivar Columbia; BAC clone F17M5
C;Genetics:
A;Gene: ATSP:F17M5.40
A;Map postition: 4
A;Introns: 37/3; 328/1; 362/3
C; Accession: T02015
R; Stoneking, T.; Smith, R.
submitted to the EMBL Data Library, November 1998
submitted to the EMBL Data Library, November 1998
A; Description: The sequence of A. thaliana T15B16.
A; Reference number: Z14488
A; Reference number: Z14488
A; Accession: T02015
A; Accession: T02015
A; Molecule type: DNA
A; Residues: 1-190 <STO>
A; Cross-references: UNIPROT: Q9ZSH7; EMBL: AF104919; NID: G3859590; PID: G3859591
A; Experimental source: cultivar Columbia
C; Genetics:
A; Map position: 44/3; 11/1
A; Note: T15B16.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----HSTGL- 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----FEDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 FTGPVKAEEPTPTPKIP-----KKRGRKKKNADPEEINSSAPRDDDPENRSKFYES 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KA 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 IPRKFSTHCKRKLPQIVTLKSPSGVTYNVGVEBDDEKTMAFRFGWDKFVKDHSLEENDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 PHKLIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWFQDGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.7%; Score 227.5; DB 2; Length 461;
Best Local Similarity 23.3%; Pred. No. 1.2e-10;
Matches 86; Conservative 63; Mismatches 139; Indels 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.8%; Score 229; DB 2;
33.3%; Pred. No. 2.8e-11;
tive 25; Mismatches 51;
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53; Conserv
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A; Reference number: A84420; MUID:20083487; PMID:10617197 A; Accession: H84437 A; Accession: H84437 A; Accession: H84437 A; Accession: H84437 A; Catture: preliminary A; Catture: preliminary A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Molecule thaliana hypothetical protein F17114.30 Cuery Match Guery Match Best Local Similarity 21.3%; Pred. No. 2e-06; Matches 72; Conservative 56; Mismatches 128; Indels 82; Gaps 13; Matches 72; Conservative 56; Mismatches 128; Indels 82; Gaps 13; Oy 6 FHKLIFSSTI-OBKRLRVPDKFVSKFKD-ELSVAVALTVPDGHVWRVGLRKADNKIWFQD 63	Db 130 LSSEDTDTGAKSEMKNTVPEGRDKGKSKVEVVEDSDDEEEDSVYSESSEFTE 182  Qy 149 VPANKGYASSAIQTLFTGPVKAEPTPTFKIPKKRGRKK
121 130 181 155 237 191 295 248	RESULT 7 T05106 hypothetical protein F28M20.170 - Arabidopsis thaliana C;5pecies: Arabidopsis thaliana (mouse-ear crees) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T05106 R;Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, G;Accession: T05106 R;Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, November 1998 A;Reference number: Z15398 A;Recession: T05106 A;Residues: 1.352 < BEV> A;Cross-references: UNIPROT:09SB80; EMBL:AL031004 A;Residues: 1.352 < BEV> A;Cross-references: UniPROT:09SB80; EMBL:AL031004 A;Residues: 1.352 < BEV> A;Cross-references: UniPROT:09SB80; EMBL:AL031004 A;Residues: 26/3; 125/1; 166/3 A;Introms: Z6/3; 125/1; 166/3 A;Note: F28M20.170 C;Superfamily: Arabidopsis thaliana hypothetical protein F28M20.180
TESULT 6 TOATOL TOATOL TO Arabidopsis thaliana TOATOL TOATOL TO Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: TO4786 C;Bevan, M.; De Haan, M.; Maarse, A.C.; Grivell, L.A.; Hoheisel, J.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999 A;Reference number: 215384 A;Accession: TO4786 A;Molecule type: DNA A;Residues: 1-389 -*ABV> A;Accession: TO4786 A;Molecule type: UNIPROT:Q98205; EMBL:AL035521 A;Cross-references: UNIPROT:Q98205; EMBL:AL035521 A;Cross-references: UNIPROT Columbia; BAC clone F10M10 C;Genetics: A;Map position: 4 A;Introns: 29/3; 154/1; 203/1; 276/1; 306/3	Query Match         9.0%;         Score 161.5;         DB 2;         Length 352;           Best Local Similarity         20.1%;         Pred. No. 1.9e-05;         Indels 123;         Gaps 15;           Matches         69;         Conservative         49;         Mismatches         102;         Indels 123;         Gaps 15;           QY         5         FFHKLI-FSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKI 59         1
Query Match	Oy 240 TNPFFRVVLRPSYLYRCCIMYLPSGFAEKYLSGIS-GFIKVQLAEKQWPVRC-LYKA 294  by 148 DLTCFSQSVTASNLTRD-LVGIPRDFAKRYGLNIGRHEIVLMDEEGNTWESEVKSYKS 204  Cy 295 GRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRV 337

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83 VWFEKGWRD-
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Matches 66; Conserv
                      Similarity
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  Query Match
Best Local S
Matches 43
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Rite: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUD:21016719; PMID:11130712
A;Status: preliminary
A;Molecule type: DNA
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A,Cross-references: UNIPROT:Q9XIB4; GB;AE005173; NID:g5430754; PIDN:AAD43154.1; GSPDB:GN
C;Accession: T05104

N; Rieger, M.; Rueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, submitted to the Protein Sequence Database, November 1998

A;Reference number: Z15398

A;Accession: T05104

A;Accession: T05104

A;Accession: T05104

A;Residues: 1-344 < ABEV>
A;Cross-references: UNIPROT:081781; EMBL:AL031004

A;Reperimental source: cultivar Columbia; BAC clone F28M20
C;Genetics:
A;Rap position: 4

A;Introns: Z6(3; 120/1; 144/1; 185/3; 224/1; 275/3
                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                60 WFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINY-HSTGLMDSAHNHFK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPANKGYASSAIQTLFTGPVKA----EEPTPTPKIPKKRGRKKKNADPEEINSSAPRDDD 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 GDSSQKVPSSSSS----VSEYR-------FLTLTVTPAALKDGRLR-VPIK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAEKYLSGISGFIKVQLAEK---QMPVR-CLYKAG-RAKFSQGWYEFTLENNLGEGDVCV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 KOSIKTELESSLDEDKVNMGKFPRKKHVKKRIPEAEAKSFSSDKSCFVAHVTDSNLREDT 184
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                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F13F21.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                   5 FFHKLI--FSSTIQEKRLRVPDKFVSK---FKDELSVAVALTVPDGHVWRVGLRKADNKI
                                                                                                                                                                                                                                                                                                                                                                                                       14 FFQPLLPGFDS----YLNIPVKFFSKRIQGRNEGRTVELRTDASEKTWQVKIQGRRLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFLPRKFDRS--DGLIKGSNKIVLMNEBARTWTLILKFRNSKLKSVSTKDFN-KIKRKES
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                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                                                                     Length 344;
                                                                                                                                                                                                                                                                                   8.1%; Score 145; DB 2; Length 34.
23.6%; Pred. No. 0.0004;
tive 51; Mismatches 146; Indels
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                                                                                                                                                                                                                                                                                                       Local Similarity 23.6% tes 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KSFVLEL 343
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A,Map position: 1
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Best Local Si
Matches 88
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hypothetical protein F28M20.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05101
R;Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ξ
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45871
R;Bloecker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanoubat, Isubmitted to the Protein Sequence Database, January 2000
A;Reference number: Z23016
A;Accession: T45871
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-283 <BLO>
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                                                                                                                                                                                                                             59 IWFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFK 118
                                                                                                                                                                                                                                                                                    -----SCFRVVIPDVSASEIEY---PLDDTDDN--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 EDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTFTPKIPKKR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127
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                                                                                                                                              24 PEPTVKKFIKIILLERIIEKAMKVPARFV-RFGPKLTDNVTLQTPVGFKRSIRIKRIGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GWOEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKRARLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRFFKVFLVESASES-LMIPLPFMAFLADPLPKTVKLOGLGGKLWTVSLKKISGAAYLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 GRKKKNADPEEINSSAPRDDPENRSKFYESASARKRTVTAEERERAINAAKTFEP---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 PFFHKLIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWFQD
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                                                             Gaps
                                                             39;
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  Length 210;
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                                                             Indels
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A;Experimental source: cultivar Columbia; BAC clone F4P12
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----ABI-----QAIPLSDSDSDSVVED---
; Score 141.5; DB 2;
; Pred. No. 0.00039;
24; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.9%; Score 141; DB 2; 1
19.8%; Pred. No. 0.00064;
iive 49; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ADKRVCFKGWDRICRRNRLKKHQDTVECELL 264
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                                                                                                                                                                                                                                                                                                                                                                                  119 RARLFEDLE-----DEDAEVI
     7.9%;
                                                             43; Conservative
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Bate: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01545
R;Andrews, S.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of A. thaliana IG005110.
A;Reference number: Z14347
A;Accession: T01545
A;Accession: T01545
A;Accession: T01545
A;Accession: T01545
A;Accession: T01545
A;Molecule type: DNA
A;Residues: 1-490 <AND.
A;Cross-references: UNIPROT:023076; EMBL:AF013293; NID:g2252823; PID:g2252835
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;Introns: 112/3; 216/1; 256/3; 391/3
A;Note: A IG005110.15
C;Superfamily: Arabidopsis thaliana hypothetical protein F28M20.180
                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 NKIWFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINY-----HSTGLMD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 SGENEISEKEGEENVQKESDKSSSDLNCFSQSVTHSNISRDAVSVPRDFV------170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 CTENKLDVGDSCTFKLLQKAKTPVFQLCSRTK-----HLPLSFTK----VNGLINP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 SAHNHFKRARLFEDLEDEDAEV----IFPSSVYPSPLPESTVPANKGYASSAIQTLFTG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 PVKAEBPTPTPKIPKKRGRKKKKNADPEEINSSAPRDDDPENRSKFYESAS---ARKRTVT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KRSGFSKGR---HEIVLMNEEGKSWESEVKSYMSGAVYLVGGWTTF 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 AEBRERAINAAKTF----EPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFI-- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 -KVQLAEK---QWPVRCLYXAGRAKFSQG---WYEFTLENNLGEGDVCVFELLR----- 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: | : | : | : | : | 261 GKIILVDKDRAEWSWALKVDSRGAVYIIGGNDWKSFCAANEVGAGESLALELIQGGVLLN 320
                                                                                                                                                                                                                                                                                                                                                                                                             14 FFQPLLPGFQS-----NLKIPVNYFSEHIEGKHEGKTVTLRTDASERTWEVKMEGHR--- 65
                                                                                                                                                                                                                                                                                                                                                                                  5 FFHKLI--FSSTIQEKRLRVPDKFVSKF---KDELSVAVALTVPDGHVWRV---GLRKAD 56
                                                                                                                                                                                                                                                                                                                                          95;
                                                                                                                                                                                                                                                Superfamily: Arabidopsis thaliana hypothetical protein F28M20.180
                                                                                                                                                                                                                                                                                               Length 461;
submitted to the Protein Sequence Database, November 1998
A;Reference number: 215398
A;Reference number: 215398
A;Reference type: DNA
A;Molecule type: DNA
A;Residues: 1-46: -8EV->
A;Cross-references: UNIPROT:081778; EMBL:AL031004
A;Experimental source: cultivar Columbia; BAC clone F28M20
C;Genetics:
A;Map position: 4
A;Introns: 26/3; 125/1; 163/3; 245/3; 316/3
A;Note: F28M20.120
C;Superfamily: Arabidopsis thaliana hypothetical protein F28M2
                                                                                                                                                                                                                                                                                             Match 7.8%; Score 140.5; DB 2; Length Local Similarity 21.5%; Pred. No. 0.0014; les 81; Conservative 50; Mismatches 151; Indels
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321 QITTCFQMEQPSFKAED 337
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Matches
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65;

Indels

22 VPDKFVSKF---KDELSVAVALTVPDGHVWRVGLRKADNKIWFQDGWQEFVDRYSIRIGY 78

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hypochhetical protein F28MZ0.180 - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress) (C;Species: Arabidopsis thaliana (mouse-ear cress) (C;Date: 23-Apr-1999 #text_change 09-Jul-2004 (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T05107) (C;Accession: T0
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A;Note: F28M20.180
C;Superfamily: Arabidopsis thaliana hypothetical protein F28M20.180
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                                                                                                                                                                  209 -HEKSWILLIRHNKKIGQAFWRGGWRSFCRNNGIKAGSICRFKLVQS 254
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A;Molecule type: DNA
A;Residuss: 1-1440 <STO>
A;Cross-references: UNIPROT:Q9SJA0; GB:AE002093; NID:g4572680; PIDN:AAD23895.1; GSPDB:GN
C;Genetics:
A;Gene: At2g24650
A;Map position: 2
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A;Residues: 1-984 <STO>
A;Cross-references: UNIPROT:Q9LQY4; GB:AE005172; NID:g9295721; PIDN:AAF87027.1; GSPDB:GN
C;Genetics:
                                                                                             Cydecesion G86393
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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  protein T24P13.6 [imported] - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C.Accession: G86393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 FPQPIL---TESRTHLNIPVAFFSKHVEGRNNQNKTVTLR-----SDASDKTWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
7.4%; Score 133.5; DB 2; Length 984;
Best Local Similarity 21.4%; Pred. No. 0.014;
Matches 81; Conservative 46; Mismatches 151; Indels 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 TLENNLGEGDVCVFELLRT 325
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A,Status: preliminary
A,Molecule type: DNA
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                                                                                        5 FFHKLIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWFQDG
                                                                                                                   10 FFHTLVPSF---HTHLMIPEDFFSEXIEGRSVAELKLDFSDKSWEVKL--SDRRI--TDG
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                                              Indels 123;
Length 1440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 VRCLYKA-GRAKFSQGWYEFTLENNLGEG 315
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Novel VRNI polynucleotide sequence encoding a polypeptide which alters vernalization response of plant in which VRNI nucleic acid is expressed, useful for influencing and assessing vernalization phenotype of plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of Arabidopsis thaliana VRNI. This protein is capable of altering the vernalisation responses of a plant. Also provided are a number of PCR primers used to isolate the sequences. The sequences are useful in the production of crop plants, where they are able to control the timing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2. .94
/label= B3_DNA_binding_domain
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/label= region_2
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Arabidopsis thaliana
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N-PSDB; AAF62446.
Levy YY;
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flowering, the duration of vernalisation required, the optimum temperature, or even eliminate the need for vernalisation completely. The present sequence is the VRN1 protein
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                                                                                                                                                                                      Length 341;
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Claim 1; SEQ ID NO 1818; 134pp; English

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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are upcommunications. Specifically, it refers to identifying genes that are upcommercially in transgenic plants oversypesshing the heterodimeric stransgenic plants for the production of growth regulators, calter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, canzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or blomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, cach relative to the corresponding wild type plants. Accordingly, these each relative to the corresponding wild type plants. Accordingly, these during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/ or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale cress protein expressed by a gene repressed 1.3 fold or more in plants oversexpressing the EZFa/DPa transcription factor, given in an exemplification of the
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 69063.
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                                                                                                AAG54186 standard; protein; 377 AA
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AAG54186
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260
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                          IFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKRARLFEDLEDEDAEVIFPSSVY
                                                                                                                                                         RDDDPENRSKFYESASARKRTVTAEERERAINAAKTFEPTNPFFRVVLRPSYLYRGCIMY
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Indels

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65.1%; Score 1170; DB 3; Length 284;
Best Local Similarity 96.1%; Pred. No. 3.6e-106;
Matches 223; Conservative 2; Mismatches 7; Indels
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99US-0160814P.
99US-0160810P.
99US-0160980P.
99US-0160981P.
99US-0161404P.
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99US-0161359P.
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99US-0123180P.
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
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19-APR-1999;
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                                                                                                                                                                                       53.1%; Score 953; DB 3; Length 182;
llarity 100.0%; Pred. No. 4e-85;
Conservative 0; Mismatches 0; Indels
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990S-0159584P.
990S-0160741P.
990S-016076P.
990S-016070P.
990S-0160814P.
990S-0160814P.
990S-0160980P.
990S-0161940P.
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Best Local Simil
Matches 181; C
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   110 MDSAHNHF-KRARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGY-ASSAIQTLFTGP 167
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                                                                                                                                                                                                                                                                             168 VKAEEPTPTPKIPKKRGRKKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEER
                                                                                                                                                                                                                             18; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                             VRCLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV 341
                                                                                                                                                                                                                                                                                                                                                     Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 79595.
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Matches 190; Conservative 14; Mismatches 18
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29-OCT-1999;
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110 MDSAHNHF-KRARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGY-ASSAIQTLFTGP 167
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                                                                                                                                                                                                                                                                                                                                                                                                 168 VKAREPTPTPKIPKKRGRKKKNADPBEINSSAPRODDPENRSKFYESASARKRTVTAEER
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                                                                                                                                                                                                                                                                                                                                          Length 224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 79594.
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81.2%; Pred. No. 2.6e-84;
ive 14; Mismatches 18;
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52.7%; Scott 3.7, 1881.2%;
Best Local Similarity 81.2%; Pred. No. 2.7e-84;
Matches 190; Conservative 14; Mismatches 18; Indels
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81.2%; Pred. No. 2.7e-84;
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Best Local Similarity 81.2%
Matches 190; Conservative
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Protein identification; signal transduction pathway; metabolic pathway;

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 hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Search completed: December 30, 2004, 06:08:56

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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## ALIGNMEN.

RESULT 1 US-09-543-681A-7819

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Sequence 7819, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIT
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
SEQ ID NO 7819
SEQ ID NO 7819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 IQEKRLR------VPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWFQDGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.4%; Score 97.5; DB 4; Length 1178; 21.7%; Pred. No. 0.47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Proteus mirabilis
US-09-543-681A-7819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 21.7
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Matches
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118 KRARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTFP 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Bach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefeky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
5.4%; Score 97; DB 4; Length 399;
Best Local Similarity 28.9%; Pred. No. 0.095;
Matches 37; Conservative 14; Mismatches 71; Indels
                                                                                                                                         CUDREAUTH TYPE: C./COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/065,598
FILING DATE: JH MAY 1998
APPLICATION NUMBER: 60/05571
FILING DATE: JH MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JH MAY 1998
APPLICATION NUMBER: 40,489
REPRENENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 6398:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                            ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-08-539-205A-6
; Sequence 6, Application US/08539205A
; Patent No. 6001619
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US-09-107-532A-6398

US-09-107-532A-6398

Sequence 6.5819. Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A DOUCELTE-Stamm and David Bush

APPLICANT: Lynn A DOUCELTE ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS

TITLE OF INVENTION:
                                     APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Sviatlo, Edwin
APPLICANT: Vother, Janet
APPLICANT: Tart, Marilyn J.
APPLICANT: Tart, Rebeca
APPLICANT: Tart, Rebeca
APPLICANT: Tart, Rebeca
APPLICANT: Brooks-Walter, Alexis
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES, TITLE OF INVENTION: PORTIONS AND PRODUCTS
TITLE OF INVENTION: PORTIONS AND PRODUCTS
CORRESPONDENCE ADDRESS:
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5.4%; Score 97.5; DB 4; Length 8991;
Best Local Similarity .24.4%; Pred. No. 12;
Matches 38; Conservative 17; Mismatches 72; Indels 29
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5769 GVOLRDAGGSNNVGAYFKEGLEETTAEXEAGLGKAE 5804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Curtis, Morris & Safford, P.C. STREET: 530 Fifth Avenue CITY: New York STATE: New York STATE: New York ZITY: U.S. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 8991 amino acids
TYPE: amino acid
STRANDEDNESS: single
Briles, David E.
McDaniel, Larry S.
Swiatlo, Edwin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: amino acid
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; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 SPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPKKRKKKKNADPEEINSSAPR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 VPEPWETISEEVNIAGDSLGLAL------PPPPVSPGSR-----TSPQELSEELSR 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 -----DDDPENRSKFYE-SASARKRTVTAEERERAINAAKTFEPTNPFFRVVLRPSYLY 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 VWRVGLRKADNKIWFQD------GWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09392163A
Patent No. 6503742
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Caligiuri, Maureen
APPLICANT: Nefeky, Bradley
TITLE OF INVENTION: Ubiquitin Ligases, and Uses Related Thereto
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.3%; Score 95.5; DB 3; Length 834; Best Local Similarity 21.0%; Pred. No. 0.45; Matches 66; Conservative 32; Mismatches 109; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPRPFFHKLIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDG-
                                                                 CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

- APPLICATION NUMBER: US/08/539,205A
FILING DATE: 04-0CT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REPRENCE/DOCKET NUMBER: CSV-005.01
TELECOMMUNICATION INFORMATION:
TELEFENDE: (617) 832-1000
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: FOLEY, HOAG & ELIOT LLP STREET: One Post Office Square CITY: Boston STATE: MA COUNTRY: USA ZIP: 02109-2170
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                             LENGTH: 834 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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RESULT 6
US-09-248-796A-15909
US-09-248-796A-15909

Sequence 15909, Application US/09248796A

FACENT NO. 6747137

GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

FRIOR APPLICATION NUMBER: US 60/074,725

FRIOR APPLICATION NUMBER: US 60/096,409

FRIOR APPLICATION NUMBER: US 60/096,409

FRIOR APPLICATION NUMBER: US 60/096,409

FRIOR APPLICATION NUMBER: US 60/096,409

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FRIOR APPLICATION NUMBER: US 60/096,409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 SPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPKKRGRKKKNADPEEINSSAPR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 VÞEPWETISEEVNIAGDSLGLAL------PPPPVSPGSR-----TSPQELSEELSR 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MERPY-----TFKDFLLR-PRSHKSRVKGFLRLKMAYMPKNGGQDEENSDQRDDMEH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 GWEV-VDSNDSASQHQEELPPPPLPPGWEEKVDNLG-------RTYYVNH 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 VWRVGLRKADNKIWFQD------GWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.3%; Score 95.5; DB 4; Length 834; Best Local Similarity 21.0%; Pred. No. 0.45; Matches 66; Conservative 32; Mismatches 109; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPRPFHKLIFSSTIGEKRLRVPDKFVSKFKDELSVAVALTVPDG--
PatentIn Release #1.0, Version #1.30
                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/392,163A
FILING DATE:
FRIOR APPLICATION DATA:
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/539,205
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: GSV-005.01
FREPERRUCE/DOCKET NUMBER: GSV-005.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-7000
TELEPAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acids
TTPE: amino acids
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Sequence 10361, Application US/09489039A

Patent No. 6610836

Patent No. 6610836

Patent No. 6610836

Patent No. 6610836

Patent No. 6610836

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Patent No. 6610836

Patent No. 6610836

Patent No. 6610836

Patent No. 6610836

Patent No. 6610836

Patent No. 6610836

Patent No. 6610836

Patent No. 6610836

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PATENT NO. 10361

PRIOR PALICATION NUMBER: US 60/117,747

PRIOR PATENT NO. 10361

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO. 10361

LENGTH: 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 DIRDED-AEVIPPSSVYPSPLPESTV---PANKGYASSAIQTLFTGPVKAEEPTPTRK-- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ы.ВРРРААОРVVEPVVEРЕРЕРЕРЕУVРЕРРКЕ------АРVVIHKPEPKPK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 PKPKPEKKVEQPKREVKPAAEPRPASPFENNNTAPARTAPST-----STAAKPTVT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 -IPKKRGRKK------KNADPEEINSSAPRDDPENRSKFYESASARKRTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEERERAINAAKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.2%; Score 93.5; DB 4; Length 274; Best Local Similarity 24.4%; Pred. No. 0.12; Matches 51; Conservative 20; Mismatches 65; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Sviatlo, Edwin
APPLICANT: Yother, Janet
APPLICANT: Yocher, Janet
APPLICANT: Processal Genes, Portions
TITLE OF INVENTION: Thereof, Expression Products
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
TITLE OF INVENTION: Portions and Products
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS: 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KVQLAEKQWPVRCLYKAGR 296
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APPLICATION NUMBER: US/08/529,055
FILING DATE: 15-5EP-1995
GIASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 64, Application US/08529055
Patent No. 6592876
GENERAL INFORMATION:
APPLICANT: Briles, David E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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Sequence 26890, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-132

CURRENT PAPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 26890

LENGTH: 693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 SLQNELEEKKSLSNDSRESSFTPFPLNMSPTLLSPNPSVNLSPTNSRNYVSFPFKAPPSS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEPTPTPKIPKKRGRKKKNADPE-EINSSAPRDDPENRSKFYESASARKRTVTAEERER 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 İRSILLIWTROYTIİDOKKKAVANNANIALLOFWSLFRVIITFTDSLOQSSMHTNHLS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 LRKADNKIWFODGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMD 111
                                                                                                                                                                                                             66 QEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKRARLFED 125
                                                                                                                                                                                                                                                                                                                 126 LEDEDAEVIFPSSVYPSPLPESTVPANKGYASSALQTLFTGPVKAEEPTPT------ 176
                                                                                                                                                                                                                                                                                                                                                 ---PKIPKKRGRKKKNADPEEINSSAPRDDDFENRSKFYESASARKRTVTAEERERAINA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                             407 FGKFSITKKRG-KHRLINKDQVSQGTINDD------FDDGVTVGQEPEPERDRDRA-NY 457
                                                                                                                                                                                                                                                       312 ------DYFHIFFRNPGDPILFDLONYQHTEVQFIQITSEDKSELHSK----- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 IFSS-----TIQEKRLRVPD-----KFVSKFKDELSVAVALTVPDGHVWRVG 51
                                                                                                              9 LIFSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVG---LRKADNKIWFQDGW 65
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                                                                 57;
                                                                                                                                                              260 LLLSNSDÓEPIRKOINFGMRDFKNFLNLANFFTTPSSSSERLDENYVTTANN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 WETPOLKNWYODLSHYFLPNASNOI--LLDHLOOHNROFDQLKMDLI----
                     Length 497;
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                                                                    95; Indels
               5; DB 4;
0.25;
                  Query Match 5.3%; Score 94.5; D
Best Local Similarity 21.0%; Pred. No. 0.25
Matches 51; Conservative 40; Mismatches
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US-09-248-796A-26890
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458 AET 460
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US-09-248-796A-26890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 PTPKIPKKRGRKKKNADPEEINSSAPRDDPENRSKFYESASARKRTVTAEERERAINAA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.2%; Score 92.5; DB 4; Length 194; Best Local Similarity 28.1%; Pred. No. 0.092; Matches 36; Conservative 17; Mismatches 56; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | September | Sequence | September | Sequence | September | Sequence | September | Sequence | September | Sequence | September | Sequence | TITLE OF INVENTION: Expressed Ligand - Vascular | TITLE OF INVENTION: Intercellular Signalling Molecule; NUMBER OF SEQUENCES: 28 | NUMBER OF SEQUENCES: 28 | STREET: 777 Old Saw Mill Road | STREET: 777 Old Saw Mill Road | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY | STATE: NY |
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Estable
COMPUTER: FastESEQ Version 2.0
SOGTWARE: FastESEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,223A
FILING DATE: 25-CT-1996
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: USN 60/022/999
FILING DATE: 02-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: CObert, Robert 3
REGISTRATION NUMBER: 36,108
REGISTRATION NUMBER: 36,108
REGISTRATION NUMBER: 36,108
REGISTRATION NUMBER: 34,108
TELEPHONE: 914-345-7721
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                        REPERENCE/DOCKET NUMBER: 454312-2400
TELECOMUNIACATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INPORMATION FOR SEQ 1D NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
REGISTRATION NUMBER: 25,506
                                                                                                                                                                                                                                                                     LENGTH: 194 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: peptide US-08-529-055-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 KTFEPTNP 242
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GENERAL INFORMATION:
APPLICANT: Davis et al.
TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule
FILE REFERENCE: REG 333-Z
CURRENT FILING DATE: 2000-11-09
PRIOR FILING DATE: 1996-10-25
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 496
                                                                                                                                                                                                                                                                 | | : | : | : | : | : | : | 319 GGGWTIIQRREDGSLDFQKGWKEYKVGFGSPSGBYWLGNEFISQIINQQRYYLKIHLKDW 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 GGGWTIIQRREDGSLDFQXGWKEYKVGFGSPSGEYWLGNEFISQITNQQRYVLKIHLKDW 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----EFVDRYSIRIGYLL---IFRY 84
                                                                                                                                                                                                                                    ----EFVDRYSIRIGYLL---IFRY 84
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Fatent No. 6703491

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 44371

LENGTH: 748
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                                                                                                                                                                                 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.2%; Score 92.5; DB 4; Length 496; Best Local Similarity 29.3%; Pred. No. 0.42; Matches 27; Conservative 16; Mismatches 26; Indels 2
                                                                                                                              Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.1%; Score 92; DB 4; Length 748; Best Local Similarity 27.2%; Pred. No. 0.91; Matches 44; Conservative 19; Mismatches 63; Indels
                                                                                                                                                                                 26; Indels
                                                                                                                              5; DB 3;
0.42;
                                                                                                                                                                                                                                                                                                                                                                     379 EGNEAYSLYDHFYISGEELNYRIHLKGLTGTA 410
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                                                                                                                                                                                                                                                                                                                                       85 EGNSAFSVY-IFNLSHSEINY--HSTGLMDSA 113
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                                                                                                                                                                                 16, Mismatches
NAME/KEY: hTL2

1 LCATION: 1...496

CTHER INFORMATION: human TIE-2 ligand 2

US-08-740-223A-16
                                                                                                                              5.2%; Score 92.5; 29.3%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 16, Application US/09709188; Patent No. 6441137
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                                                                                                                                                      Best Local Similarity 29.3%
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-270-767-44371
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US-09-709-188-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 SSSILEKHLITSRKLLHHH-----SAVNDDDARVLLEFANSKOPPLAASSTTFVVNA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          768 DG--WYGALKEAVQQQQNQLVWVSEGKADGATSDDLDLHDDRLSYL----SAPGSEYSMY 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----VYP------SPLPESTVPANKGYASSAI-QTL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 FTGPVKAEEPTPTPKIPKKRGRKKKWADPEEINSSAPRDDDPENRSKFYESASARKRTVT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 AEERERAINAAK-----TFEPTNPFF----RVVLRPSYLYRGCIMYL 261
                                                                          152 NKGYASSAIQTLFTGPVKAEEPTPTPKIPKKRGRK----KKNADPEEINSSAPRDDDPEN 207
                                                                                                                589 SVGFPSA-----GSVFASSSTSCSKAPAKPGEEYILPDNNMDVDEIVIS-----S 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09762481B
Patent No. 6632639
GENERAL INFORMATION:
APPLICANT: DIREYTGS, MARC
APPLICANT: LOPEZ, PASCAL
TITLE OF INVENTION: WITNIT E. COLI STRAINS, AND THEIR USE FOR PRODUCING
TITLE OF INVENTION: RECOMBINANT POLYPEPTIDES
FILE REFERENCE: USB98APCNREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 DGHVWRVGLRKA-----DNKIWFQDG-----WQEFVDRYSIRIGYLLIFRYEGNSAFSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         822 STDSRHTS-DYEDT---DIEGGAYTDQELDETLNDEVGTPPESAITRSSEPVREDSSGMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT MALLEY, George L.

TITLE OF INVENTION:
FILE REFERENCE: B0801/7225
CURRENT PEPLICATION NUMBER: US/09/919,497
CURRENT PEPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
SHSEINYHSTGLMDSAHNHFKRARLFEDLEDEDAEVI--FPSSVYPSPLPEST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.1%; Score 91.5; DB 4; Length 1736; Best Local Similarity 19.4%; Pred. No. 4; Matches 63; Conservative 41; Mismatches 126; Indels 95;
                                                                                                                                                           208 RSKFYESASARKRTVTAEE----RERAINAAKTFEPTNPFFR 245
                                                                                                                                                                                                 634 SSSYTSSAAQVQNTLQPPDFNFLYHQATTTATTATYFNPFSR 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1055 TDQFSRNYEHRLRYEDRVPMYEEQW 1079
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                                                                                                                                                                                                                                                                                                Sequence 98, Application US/09919497
Patent No. 6773883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Homo sapiens
US-09-919-497-98
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US-09-919-497-98
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510 MALPSEEBFABRKRPEQPALATFAMPDVPPAPTPABPAAPVVAPAPKAAPATPAAPAQPG 569
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                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                     5.0%; Score 90; DB 4; Length 1061; 22.9%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                        93 YIFNLSHSEINYHST------GLMDSAHNHFKRARLFEDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 RSKFYESASARK------RTVTAEERERAINAAKT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           626 RSERTEGSDNREENRRNRRQAQQQTAETRESRQQAEVT 663
                                                                                                                                                                                                                                                                                                                                                  69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: 3.5 inch, 1.44 Mb floppy disk
IBM PC compatible
CURRENT APPLICATION NUMBER: US/09/762,481B;
CURRENT FILING DATE: 2001-08-27;
PRIOR APPLICATION NUMBER: PCT/FR99/01879;
PRIOR FILING DATE: 1999-07-29;
PRIOR FILING DATE: 1998-08-07;
NUMBER OF SEQ ID NOS: 6;
SEQ ID NOS: 6;
SEQ ID NO 2;
SEQ ID NO 2;
                                                                                                                                                                                                                                                                                                                                                  21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08960507; Patent No. 6057435; GENERAL INFORMATION: GENERAL THORNATION: APPLICANT: GOGOWSKI, Paul J. APPLICANT: GUTNEY, Austin L. TITLE OF INVENTION: Tie Ligands; NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS: ADDRESSES: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P1130p1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INPORMATION:
ATMAR: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 amino acids
Amino Acid
                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-762-481B-2
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: WinPat
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
TOPOLOGY:
US-08-960-507-20
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us-10-088-187a-11.rai
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Query Match 4.9%; Score 88.5; DB 3; Length 286;
Best Local Similarity 30.4%; Pred. No. 0.47;
Matches 28; Conservative 14; Mismatches 27; Indels 23; Gaps 4;
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Search completed: December 30, 2004, 06:15:51 Job time : 27 secs

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December 30, 2004, 06:10:48 ; Search time 367 Seconds (without alignments) 334.243 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1599051 segs, 359727711 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*
                                                                                                                                                               - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                               OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |     |        |             | 260947,              | 240434,              | 240433,              | 9287, Ap           | 274348,              | 63507, A            | 157411,              | 166413,              | 192114,              | 78183,               | 203869,              | 152254,              | 129669,              |
|-----------|-----|--------|-------------|----------------------|----------------------|----------------------|--------------------|----------------------|---------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|----------------------|
| SUMMARIES | مان |        | Description | Sequence 2           | Sequence 2           | Sequence 2           | Sequence 9         | Sequence 2           |                     | Sequence 1           | Sequence 1           | Sequence 1           | Sequence 1           | Sequence 2           |                      | Sequence 1           |
|           |     |        | ID          | US-10-424-599-260947 | US-10-424-599-240434 | US-10-424-599-240433 | US-10-739-930-9287 | US-10-425-115-274348 | US-10-425-114-63507 | US-10-437-963-157411 | US-10-424-599-166413 | US-10-437-963-192114 | US-10-437-963-178183 | US-10-437-963-203869 | US-10-437-963-152254 | US-10-437-963-129669 |
|           |     |        |             | 15                   | 15                   | 15                   | 11                 | 17                   | 15                  | 16                   | 15                   | 16                   | 16                   | 16                   | 16                   | 16                   |
|           |     |        | Length I    | 431                  | 188                  | 203                  | 344                | 502                  | 375                 | 402                  | 181                  | 362                  | 750                  | 737                  | 322                  | 306                  |
|           |     | Query  | Match       | 50.6                 | 30.9                 | 20.9                 | 18.3               | 16.1                 | 15.6                | 15.5                 | 14.8                 | 14.8                 | 14.0                 | 13.7                 | 13.4                 | 11.9                 |
|           |     |        | Score       | 908.5                | 554.5                | 375.5                | 329                | 289.5                | 280                 | 278                  | 266.5                | 265                  | 251.5                | 246                  | 241.5                | 214                  |
|           |     | Result | No.         | 1                    | 7                    | Ю                    | 4                  | S                    | 9                   | 7                    | æ                    | σ                    | 10                   | 11                   | 12                   | 13                   |

ઠે 셤 ò 셤 à

| Sequence 206969,<br>Sequence 1314879,<br>Sequence 137150,<br>Sequence 173784,<br>Sequence 12720,<br>Sequence 12720,<br>Sequence 195577,<br>Sequence 232448,<br>Sequence 120554,<br>Sequence 120554,                                            | 96957<br>138427<br>15691<br>241659<br>42561<br>10566<br>18875<br>27434<br>17045<br>20720                                                                                                 | 18890<br>29203<br>253853<br>122653<br>341148<br>16714<br>35835<br>17395<br>54013                |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------|
| US-10-424-599-206969<br>US-10-425-115-314879<br>US-10-437-963-1187150<br>US-10-437-963-1187150<br>US-10-434-599-179398<br>US-10-437-963-162720<br>US-10-437-963-1265577<br>US-10-424-599-222448<br>US-10-437-963-120554<br>US-10-437-963-17245 | 0-739-930-9695<br>0-437-963-13842<br>0-424-599-24199<br>0-424-599-21659<br>0-425-114-4261<br>0-437-963-11875<br>0-437-963-11045<br>0-437-963-11045<br>0-437-963-11045<br>0-437-963-11045 | 10-437-<br>10-425-<br>10-425-<br>10-437-<br>10-425-<br>10-425-<br>10-425-<br>10-425-<br>10-425- |
|                                                                                                                                                                                                                                                |                                                                                                                                                                                          | <del></del>                                                                                     |
| 164<br>396<br>519<br>1355<br>118<br>536<br>462<br>100<br>538<br>538                                                                                                                                                                            | 167<br>391<br>270<br>270<br>352<br>305<br>305<br>230<br>141<br>141                                                                                                                       | 255<br>105<br>212<br>237<br>239<br>239<br>1070<br>126<br>156<br>148                             |
|                                                                                                                                                                                                                                                |                                                                                                                                                                                          | ######################################                                                          |
| 210.5<br>204.5<br>197.<br>195.5<br>193.5<br>193<br>186<br>175.5                                                                                                                                                                                | 171.5<br>170.5<br>16.5<br>16.5<br>16.2<br>16.2<br>14.1<br>14.1<br>140.5                                                                                                                  | 140<br>135.5<br>135.5<br>134<br>128.5<br>127.5<br>123.5                                         |
| 11111222222222222222222222222222222222                                                                                                                                                                                                         | 4 4 2 4 2 4 2 4 2 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                  | W W W W A A A A A A<br>O C B D O U U W A R                                                      |

## ALIGNMENTS

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Sequence 260947, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION OF 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CFLDGWKGFVQRYSIGVGSLCVRTRVGKSVRTVVJFNLATSEINYQSVTRSSNEGLHFTN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 WFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 A-RLFEDLEDEDAEVI---FPSSVYPSPLP-----ESTVPANKGYASSAIQTLFTG- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MPHPSFHKLILDSTVQPNQQLRLPDNFWRKYGGELSPIVTLSVPDGSVWHVGLKKADNKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MPRPFFHKLIFSSTIQ-EKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.6%; Score 908.5; DB 15; Length 431; Best Local Similarity 49.7%; Pred. No. 7.1e-76; Matches 198; Conservative 46; Mismatches 95; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_77658C.1.pep
US-10-424-599-260947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine max
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155

241

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Sequence 9287, Application US/10739930

Publication No. US20040216190A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: UNCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: 19.213771 BS
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT PILING DATE: 2003-12-18
SEQ ID NOS: 11088
SEQ ID NOS: 11088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PTEI----HRSGO 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 FKSCNPFFLTVMHRTHISSHGSLANLPMKFCRSHLDLHKKRRLISLQVLSGRIWFAKYQIH 265
                                                                                                                                                                                                                                                                                                                      16 FFXIITAHNVHEGKLMIPNKFVKKYGKRLQNTLFLKTPNGAEWKMILKKRDGKIWFQKGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 QEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKRARLFED
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                                                                                                                                                                                                                                                                                          182 KRGRKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEERERAINAAKTFEPTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 FHKLIFSSTIQEKRLRVPDKFVSKPKDELSVAVALTVPDGHVWRVGLRKADNKIWFQDGW
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                Length 203;
                                                                                                                                                                                                                                                                                                                                                                             242 PFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAE-KQWPV 288
                                                                                                                                                                                                                                                                                                                                                                                                  Length 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: GLYMA-23APR03-C63260_1.p
US-10-739-930-9287
                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_59138C.1.pep
US-10-424-599-240433
                                                                                                                                                                                                              20.9%; Score 375.5; DB 15; 68.5%; Pred. No. 1.4e-26; tive 14; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.3%; Score 329; DB 17; 27.2%; Pred. No. 6.4e-22; tive 57; Mismatches 130;
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 240433
LENGTH: 203
                                                                                                                                                                                           Query Match
Best Local Similarity 60.--
Best A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94; Conservative
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ORGANISM: Glycine max
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                                                                                           TYPE: PRT
ORGANISM: Glycine
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Sequence 240434, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 240433, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Anous Thomas J
APPLICANT: Covalic David K
APPLICANT: Covalic David K
APPLICANT: Cov Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                 241 RKKRKSDGGE--PSAGHEBEVEMRFRFYESASARKRTVTAEERERVINEAKAFEPSNPFC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 YLPSGFAEKYLSGISGFIKVQLAE-KQWPVRCLYKAGRAKFSQGWYEFTLENNLGEGDVC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PVKAEEPTPTPKI-----PKKRG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 DSENVADKPWRFYELASARKSTVTAEERERAINASKTFEPTNPFCRVVLRPSYLYRGCIM 66
        CLKFFEEMEGEDSIEISDSSPSHLSPSSLQNQALAGSVDKMPGKSYNTPPALQNLFNGS
                                                                                                                                                                                                                                                          299 RVVLRPSYLYRGCIMYLPSCFAEKHLNGVSGFIKLQISNGRQWPVRCLYKGGRAKLSQGW
                                                                                                                                                      RKKKNADPEEINSSAPRDDDPENRSKFYESASARKRTVTAEERERAINAAKTFEPTNPFF
                                                                                                                                                                                                                                       RVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAE-KQWPVRCLYKAGRAKFSQGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 DPENRS----KFYESASARKRTVTAEERERAINAAKTFEPTNPFFRVVLRPSYLYRGCIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 30.9%; Score 554.5; DB 15; Length Best Local Similarity 76.6%; Pred. No. 2.5e-43; Matches 108; Conservative 14; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_59139C.1.pep
US-10-424-599-240434
                                                                                                                                                                                                                                                                                                                                           359 FEFSLENNLGEGDVCVFELLRMKEVVLQVTIFHVTEDV 396
                                                                                                                                                                                                                                                                                                                    304 YEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRVNEYV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 VFELLRTRDFVLKVTAFRVNE 339
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US-10-424-599-240433
                               121
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RESULT

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ORGANISM: Oryza sativa
                                                                                              TYPE: PRT
ORGANISM: Zea mays
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                                                             APPLICANT: IN CONTINUE.

APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 274348
LENGTH: 502
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APPLICANT: Xovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabasks, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 PQFFKVFFPEQSTE-RLRIPTMFNQHLKEQQPTGAVSLRGPSGNRWQAALASESESEAAW 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 CFDQGWKEFVTDHSLRLGHFLVFTRDGPAQFSVAVFS-----SSGVIDPAALDARP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 TANGGAAVKLEEGEGVGVRGDVDAGGDTSSEVSILPAEEGDGGATGRRTGATSGAGGAS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 NPTFSLLDESKTFNKTQIRDKNVPRSGKFLLRTTKAPVVISQRRVTEEEKCLALRKAME 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 - PODGWOEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSA---- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 -HNHFKRARLFE-----DLE---DEDAEV-IFPSSVYPSPLPESTVPANKGYASSAI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 QTLF-----TG-----PVKAEEPTPTPKIPKKKKNA------ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 EMSLVLREEGRGVTGKRARATTSDLPADASAPKKHSALAKKAGKRRPQAATSKDVSMIVH 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----DPEEINSSAPRDDDFENRSKFYESAS-----ARKRTVTAEERERAINAAKT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 FEPTINPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAE---KQWPVRCLYK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 PKSKHPPTMQIMIBSYVYVGPPMNIACEFVRESLPRTSK--KMTLWDPMGKPWDVSYVKR 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 PPFHKLIFSSTIQEKRLRVPDKFVSKFKDELSV-AVALTVPDGHVWRVGL--RKADNKIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       446 RPRRRLLRXGWGRFALGNNLEXSDVCVFELFEEDN---MRVHIYRV 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 AGRAKFSQ-GWYEFTLENNLGEGDVCVFELLRTRDFVLKVTAFRV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.1%; Score 289.5; DB 17; Length Best Local Similarity 26.2%; Pred. No. 5.2e-18; Matches 106; Conservative 59; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEATURE:
OTHER INFORMATION: Clone ID: MRT4577_181795C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)..(502)
OTHER INFORMATION: unsure at all Xaa locations
Sequence 274348, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 63507, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
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US-10-425-114-63507
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APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-2153221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 157411
LENGTH: 402
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15.6%; Score 280; DB 15; Length 37
Best Local Similarity 27.7%; Pred. No. 2.7e-17;
Matches 89; Conservative 54; Mismatches 136; Indels
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15.5%; Score 278; DB 16; Length 40
Best Local Similarity 26.8%; Pred. No. 4.6e-17;
Matches 103; Conservative 57; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: UC-ZMFLB73255A02_FLI.pep
US-10-425-114-63507
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US-10-437-963-157411
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Publication No. US20040123343A1
GENERAL INPORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 63507
LENGTH: 375
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ORGANISM: Oryza sativa
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345 IYRV 348
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalatic David K
APPLICANT: Kovalatic David K
APPLICANT: A Congrei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 166413
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                                   53 RKADNKIWFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDS 112
                                                                                                                                                                                148 TVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPK------KRGRKKKNADPEEIN- 196
                                                                                                                                                                                                                  192 TAVKNEEDADE----LPVCELPASSASPPRHVPEGALDADGGAARRGAAKTRSLQDDLAL 247
                                                                                                                                                                                                                                                                              248 ASIP----PSIRR--YKGYVSRRRAVATAERQRATEIAHAFRSPLPYCVIRMSTMHYYYS 301
                                                                                                                                                                                                                                                                                                                                                  302 FMMRFPTGFSRQHLPRERTDVVLRDPGGKVWSV--LYIPNTRDRLSRGWCAFARGNCLEE 359
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18 RPHFFKVLVGDF--KQRLKIPPNFCKHIPWEESRKAKGLKEASMAATLEGPSGRTWLVVI
                                                        SSAPRDDDPENRSKFYESASARKRTVTAEERERAINAAKTFEPTNPFFRVVLRPSYLYRG
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14.8%; Score 266.5; DB 15; Length 181;
Best Local Similarity 34.4%; Pred. No. 1.8e-16;
Matches 64; Conservative 33; Mismatches 66; Indels 23;
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US-10-424-599-166413
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Publication No. US20040031072A1
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ORGANISM: Glycine max
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US-10-437-963-192114
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Sequence 192114, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Eco, Yongwei

APPLICANT: APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: W. Wei

APPLICANT: Harbaruk, Brad

APPLICANT: Buckharov, Andrey A.

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 12003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 192114

LENGTH: 362
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Sequence 178183, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Each, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
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US-10-437-963-192114
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APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221)
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 152254
    | | :: | : | | : | | : | | : | 338 FVAVWKKSNVTRQPCYVAISRKYANEYPEGEDQMLTLQRHGKRWQVKFCISKRKLRMLSK 397
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                                                                                                   207 WAEFANSHDIKMGDFLVFRYTGNSQFEVKIFDPS-----GCVKAASHNAVNIGQHA 257
                                                                                                                                                              124 EDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPKKR 183
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                                                                                                                                                                                                                                                                                                                                                     FRVVLRPSYLYR-GCIMYLPSGFAEKYLSGISGFIKVQLAEKQWPVR-CLYKAGRAKFSQ 301
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; Sequence 152254, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 ADPEEINSSAPRODOPENRSKFYESASAR--KRTVTAEERERAINAAKTFEPTNPFFRVV 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : |:: : || :: | | || 638 IHSSHVRSSKYCIVGVSPEPAGKYLGAVEREVVLERASRGGEWHVPFVHRQNTRGFYGAG 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                             45;
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                                                                                                                                                                                                                                                                           ch 14.0%; Score 251.5; DB 16; Length 750; I Similarity 26.9%; Pred. No. 3.2e-14; 86; Conservative 55; Mismatches 134; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
13.7%; Score 246; DB 16; Length 737;
Best Local Similarity 23.8%; Pred. No. 1e-13;
Matches 74; Conservative 60; Mismatches 123; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_99011C.1.pep
US-10-437-963-203869
                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: PAT_MRT4530_75764C.1.pep
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 178183
LENGTH: 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 203869, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 WYEFTLENNIGEGDVCVFEL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           698 WROFAGDNRLVAHDVCLFEL 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                            ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                 US-10-437-963-178183
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Shou, Youguei
TITLE OF INVENTION: Plante
FILE REPERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
LENGTH: 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 WFQDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 ARLFEDLEDEDAEVIFPSSVYPSPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----QLNTKKQQETPPI 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 PKKRGRKKKNADPEE-----INSSAPRDDDPENRSKFYESASARKRTVT-AEERERAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 RPFFHKLIFSSTIOEKRLRVPDKFVSKFKDE--LSVAVALTV-PDGHVWRVGLRKADNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                        2 PRPFFHKLIPSSTIQEKRLRVPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWF
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206969
LENGTH: 164
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                                                                                                                                                                                                                                                                                                                                             DB 15; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 QKGWKEFATYYSLDHGHLLFFEYEGTSHFDVHIFDSSALEIDYPSHG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 QDGWQEFVDRYSIRIGYLLIFRYEGNSAFSVYIFNLSHSEINYHSTG 108
                                                                                                                                                                                                                                                                                                                                                                                          Indels
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US-10-424-599-206969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.4%; Score 204.5; DB 17; Best Local Similarity 22.2%; Pred. No. 3.2e-10; Matches 76; Conservative 52; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                        Query Match 11.7%; Score 210.5; DB 15; Best Local Similarity 42.1%; Pred. No. 2.6e-11; Matches 45; Conservative 18; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: MRT4577_50230C.1.pep
US-10-425-115-314879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(396)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 314879, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
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US-10-437-9669

US-10-437-9669

Sequence 129669, Application US/10437963

Sequence 129669, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Wu, Wei

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF SEGURES 38-21(5322)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 129669

LENGTH: 306
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 PSEEGLKAELVPGCILPSRTDLTRLQKUILIEKVKAINSETPIYGYVMNNSSIHGIPCTV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRYEGNSAFSVYIFNLSHSEINYHSTGLMDSAHNHFKRARLFEDLEDEDAEVIFPSSVYP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 SPLPESTVPANKGYASSAIQTLFTGPVKAEEPTPTPKIPKKRGRKKKONADPEEINSSAPR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ------SSGCEKVCEKPVDMSGRSYDIAMRNSQDEKKKRKQRDISRQGTVK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 DDDPENRSKFYESASARKRT-VTAEERERAINAAKTFEPTNPFFRVVLRPSYLYR-GCIM 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 YLPSGFAEKYLSGISGFIKVQLAEKQWPVR-CLYKAGRAKFSQGWYEFTLENNLGEGDVC 318
             239 SQTVDICREYADVYLPFKELNMTLQRHGKNWEVLCRTKDTRTKRLSTGWSRFAQENNLQV 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 VPDKFVSKFKDELSVAVALTVPDGHVWRVGLRKADNKIWFQDGWQEFVDRYSIRIGYLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
11.9%; Score 214; DB 16; Length 306;
Best Local Similarity 19.7%; Pred. No. 2.9e-11;
Matches 63; Conservative 55; Mismatches 137; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_31904C.1.pep
US-10-437-963-129669
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                                                                                                                299 GDICLFELLKKKEYSMNV 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-10-424-599-206969
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| 233 AAKTFEPTNPFFRVVLRPSYLYRGCIMYLPSGFAEKYLSGISGFIKVQLAEK 284 | 319 V | 285 QMPVR-CLYKAGRAKFSQGWYEFTLENNLGEGDVCVFELLRTR 326 | 344 SWQVRGTAYKWHRYIIGVGWKSFCQDNRLKAGDLCAFNIEXR 386 |
|--------------------------------------------------------------|-------|-----------------------------------------------------|----------------------------------------------------|
| 233                                                          | 319   | 285                                                 | 344                                                |
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